

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 19, 2004, 21:57:03 ; Search time 73.9837 Seconds  
(without alignments)  
504.271 Million cell updates/sec

Title: US-10-674-755-21

Perfect score: 518

Sequence: 1 LAKKQTELEKLDLNDLPEKGK.....TKELDALNELGPDGDEE 104

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

A\_Geneseq\_23Sep04:\*  
1: geneseq1980s:\*  
2: geneseq1990s:\*  
3: geneseq2000s:\*  
4: geneseq2001s:\*  
5: geneseq2002s:\*  
6: geneseq2003as:\*  
7: geneseq2003bs:\*  
8: geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	508	98.1	213	7	ABW02601
2	508	98.1	8991	6	ABU08487
3	506	97.7	213	2	AAW14567
4	484	93.4	416	8	ADK52498
5	484	93.4	526	8	ADK52497
6	484	93.4	744	6	ABU00449
7	484	93.4	744	6	ADM92054
8	484	93.4	745	3	AAV1652
9	483	93.2	641	2	AAW1217
10	483	93.2	641	5	ABP54636
11	483	93.2	641	7	ADK45241
12	480	92.7	197	7	ABW02598
13	459	88.6	233	7	ABW02606
14	456.5	88.1	196	2	AAW14564
15	452	87.3	213	7	AAW14572
16	431	82.0	211	7	ABW02621
17	321	62.0	238	2	AAW14587
18	315	60.8	232	7	ABW02624
19	315	60.8	275	8	ADOS2055
20	315	60.8	369	8	ADK52496
21	315	60.8	458	2	AAW14552
22	315	60.8	458	7	ABW02626
23	315	60.8	653	8	ADK52495
24	315	60.8	653	8	ADOS2080
25	306	59.1	212	2	AAW14588

## ALIGNMENTS

26	306	59.1	212	7	ABW02622	Abw02622 Bg7817c p
27	304.5	58.8	233	2	AAW14590	Aaw14590 Streptoco
28	277	53.5	185	7	AD015316	Ad015316 S.pneumo
29	259	50.0	185	7	ABW02623	Abw02623 Bg7561c p
30	242.5	46.8	184	2	AAW14589	Aaw14589 Streptoco
31	199.5	38.5	487	8	ADR04321	Adr04321 Streptoco
32	199.5	38.5	489	8	ADOS2088	Ados2088 Streptoco
33	199.5	38.5	524	8	ADOS2082	Ados2082 E. coli B
34	199.5	38.5	627	8	ADOS2129	Ados2129 E. coli B
35	192.5	37.2	119	2	AAW146291	Aaw146291 Pneumono
36	192.5	37.2	215	7	AAW14563	Aaw14563 Streptoco
37	192.5	37.2	215	7	ABW02597	Abw02597 Atcc6303c
38	187.5	36.2	290	8	ADOS2119	Ados2119 pYA3637 b
39	187.5	36.2	298	8	ADOS2127	Ados2127 pYA3637 b
40	183	35.3	230	8	ADOS2086	Ados2086 S. pneumo
41	183	35.3	230	8	ADR04319	Adr04319 Streptoco
42	129.5	25.0	550	8	ADK48356	Adk48356 Streptoco
43	128	24.7	315	2	AAV04375	Aav04375 Streptoco
44	128	24.7	619	2	AAW63437	Aaw63437 Pneumococ
45	128	24.7	619	2	AAW87598	Aaw87598 Pneumococ

RESULT 1  
ABW02601  
ID ABW02601 standard; protein; 213 AA.

XX ABW02601;

DT 12-FEB-2004 (first entry)

DE Bg8090c pneumococcal surface protein A (PspA) central region.

KM Pneumococcal surface protein A; PspA; diagnosis; antigenic; vaccine;

KW immunological; gene therapy; immunostimulant.

OS Unidentified.

FH Key Location/Qualifiers

FT Misc-difference 2 /label= Unknown

PN US6592876-B1.

PD 15-JUL-2003.

XX 15-SEP-1995; 95US-00529055.

PR 20-APR-1993; 93US-00048896.

PR 06-JUN-1995; 95US-00465746.

PA (UABR-) UAB RES FOUND.

PI Briles DE, McDaniel LS, Swiatlo E, Yocher J, Brooks-Walter A;

DR WPI; 2003-862841/80.

Immunological composition for obtaining expression products used for detecting the presence of Streptococcus pneumoniae or its strain, comprises at least two different full length isolated gene encoding pneumococcal surface protein A.

Example 6; SEQ ID NO 47; 121pp; English.

The present invention relates to an immunological composition comprising at least 2 different full length isolated genes encoding pneumococcal surface protein A (PspA) from different groups based on restriction fragment polymorphism analysis. The invention is useful for obtaining expression products by recombinant techniques to detect, determine, isolate or diagnose the presence of Streptococcus pneumoniae or its strain. The expression product is useful for preparing antigenic,

CC immunological or vaccine compositions, for eliciting antibodies, an  
 CC immunological response (other than or additional to antibodies) or a  
 CC protective response (including antibody or other immunological response  
 CC by administering compositions to a host). The invention is also useful as  
 CC vaccines and in gene therapy. The present sequence is Bg8090c  
 CC pneumococcal surface protein A (PspA) central region. This sequence is  
 CC used in the exemplification of the invention  
 XX  
 SO Sequence 213 AA;  
 Query Match 98.1%; Score 508; DB 7; Length 213;  
 Best Local Similarity 98.1%; Pred. No. 1.5e-37;  
 Matches 102; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 LAKKQTELEKLDNLDPGKTDDELDEKAFAEIDKKADELPNKVADLEKEISNLEITLG 60  
 DB 59 LAKKQTELEKLDNLDPGKTDDELDEKAFAEIDKKADELPNKVADLEKEISNLEITLG 118  
 QY 61 GADPEDDTAALPNKLTATKKALEKTKQKELDPAALNELGPDGDEE 104  
 DB 119 GADPEDDTAALPNKLTATKKALEKTKQKELDPAALNELGPDGDEE 162  
 RESULT 2  
 ABU08487 standard; protein; 8991 AA.  
 XX  
 AC ABU08487;  
 XX  
 DT 24-JUN-2003 (first entry)  
 XX  
 DE S. pneumoniae pneumococcal surface protein A (PspA) protein.  
 XX  
 KM Pneumococcal surface protein C; PspC; pneumococcal surface protein A;  
 KM alpha-helical; proline rich; repeat region; pneumococcal infection; PspA;  
 KM antibacterial.  
 XX  
 OS Streptococcus pneumoniae.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 1. .8991  
 FT /note= "All Xaa residues within this sequence are  
 FT unknown"  
 XX  
 PN US6500613-B1.  
 PD 31-DEC-2002.  
 XX  
 XX 16-SEP-1996; 96US-00714741.  
 PF  
 XX 15-SEP-1995; 95US-00529055.  
 PR  
 XX (UTAL-) UNIV ALABAMA.  
 PA  
 PI Briles DE, McDaniel LS, Swiatlo E, Yother J, Crain MJ;  
 PI Hollingshead S, Tart R, Brooks-Walter A;  
 PI  
 XX WPI; 2003-361534/34.  
 DR  
 XX Isolated PspC amino acid sequence used as polymerase chain reaction or  
 PT hybridization probe, comprises pneumococcal surface protein having alpha-  
 PT helical, proline rich and repeat regions.  
 PT  
 XX Disclosure; Col 145-188; 186pp; English.  
 PS  
 XX The present invention relates to the isolation of Streptococcus  
 CC pneumoniae pneumococcal surface protein C (PspC), and the polynucleotide  
 CC sequence encoding it. PspC is a pneumococcal surface protein A (PspA)-  
 CC like protein having alpha-helical, proline rich and repeat regions. The  
 CC PspC and PspA proteins may be used in a vaccine to protect against  
 CC pneumococcal infections. The polynucleotide sequences encoding PspC and  
 CC PspA may be used for the expression of the proteins, and as PCR primers  
 CC or hybridisation probes. The present sequence represents S. pneumoniae

CC PspA protein  
 XX  
 SO Sequence 8991 AA;  
 Query Match 98.1%; Score 508; DB 6; Length 8991;  
 Best Local Similarity 98.1%; Pred. No. 1.1e-35;  
 Matches 102; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 LAKKQTELEKLDNLDPGKTDDELDEKAFAEIDKKADELPNKVADLEKEISNLEITLG 60  
 DB 4625 LAKKQTELEKLDNLDPGKTDDELDEKAFAEIDKKADELPNKVADLEKEISNLEITLG 4684  
 QY 61 GADPEDDTAALPNKLTATKKALEKTKQKELDPAALNELGPDGDEE 104  
 DB 4685 GADPEDDTAALPNKLTATKKALEKTKQKELDPAALNELGPDGDEE 4728  
 RESULT 3  
 AAW14567 standard; protein; 213 AA.  
 XX  
 AC AAW14567;  
 XX  
 DT 17-OCT-2003 (revised)  
 DT 28-OCT-1997 (first entry)  
 XX  
 DE Streptococcus pneumoniae PspA central region.  
 XX  
 KM PspA; pneumococcal surface protein; vaccine; otitis media; meningitis;  
 KM bacteraemia; pneumonia.  
 XX  
 OS Streptococcus pneumoniae; strain Bg8090.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 2 /note= "unidentified amino acid"  
 FT  
 XX W09709994-A1.  
 PN  
 PD 20-MAR-1997.  
 XX  
 XX 16-SEP-1996; 96WO-US014819.  
 PF  
 XX 15-SEP-1995; 95US-00529055.  
 PR  
 XX (UNBR-) UAB RES FOUND.  
 PA  
 PI Briles DE, McDaniel LS, Swiatlo E, Yother J, Crain MJ;  
 PI Hollingshead S, Tart R, Brooks-Walter A;  
 PI  
 XX WPI; 1997-202002/18.  
 DR  
 XX Streptococcus pneumoniae surface protein PspC and truncated PspA - used  
 PT in vaccines for protecting animals against S.pneumoniae infection.  
 PT  
 XX Example 6; Fig 13; 296pp; English.  
 PS  
 XX This sequence shows the central portion, including the C-terminus of the  
 CC alpha-helix region and some of the proline-rich region, of pneumococcal  
 CC surface protein A (PspA) of Streptococcus pneumoniae strain Bg8090.  
 CC Comparison of the N-terminal and central regions (AAW14533-57 and  
 CC AAW14562-91) of PspA polypeptides from different pneumococcal strains can  
 CC be used to divide the strains into several families based on sequence  
 CC homologies. PspA polypeptides, or fragments of them, can be used in  
 CC vaccines to protect animals against S. pneumoniae infection and hence for  
 CC the prevention of diseases such as otitis media, meningitis, bacteraemia  
 CC and pneumonia. The sequence of the 3' half of the PspA alpha-helical  
 CC region and the immediate 5' tip of the coding sequence are likely to be  
 CC the critical sequences for predicting PspA cross-reactions and vaccine  
 CC composition. (Updated on 17-OCT-2003 to standardise OS field)  
 XX  
 SO Sequence 213 AA;

Query Match 97.7%; Score 506; DB 2; Length 213;  
 Best Local Similarity 98.1%; Pred. No. 2.2e-37;  
 Matches 102; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LAKKQTELEKLDNDPBGKTODELDKEAAEAELDKKADLPNKVADLEKEISNLEILLG 60  
 DB 59 LAKKQTELEKLDNDPBGKTODELDKEAAEAELDKKADLPNKVADLEKEISNLEILLG 118

QY 61 GADPEDDTAALPNKLTATKKAELKTKQKELDAALNLELGPDDDEE 104  
 DB 119 GADPEDDTAALPNKLTATKKAELKTKQKELDAALNLELGPDDDEE 162

RESULT 4  
 ADK52498  
 ID ADK52498 standard; protein; 416 AA.

ADK52498;

20-MAY-2004 (first entry)

alpha helical region PspA molecule from the EF3296 strain.

Streptococcus pneumoniae infection; pneumococcal surface protein A; PspA;  
 hemolytic anemia disease; leukemia; lymphoma; sickle cell anemia;  
 Hodgkin's disease.

Streptococcus pneumoniae.

WO2004016231-A2.

26-FEB-2004.

17-FEB-2003; 2003WO-US008199.

15-MAR-2002; 2002US-0365351P.

(UABR-) UAB RES FOUND.

Briles DE;

WPI; 2004-192068/18.

Treating Streptococcus pneumoniae infection in a subject lacking a  
 functional spleen comprises administering an antibody that recognizes  
 pneumococcal surface protein A (PspA) or its binding portion.

Claim 17; SEQ ID NO 4; 41pp; English.

The present invention relates to treating Streptococcus pneumoniae  
 infection in a subject lacking a functional spleen comprises  
 administering an antibody that recognizes pneumococcal surface protein A  
 (PspA) or its binding portion. The method is useful for treating or  
 preventing Streptococcus pneumoniae infection in a subject lacking a  
 functional spleen. The disease-associated injury is especially due to  
 hemolytic anemia disease, leukemia or lymphoma, especially sickle cell  
 anemia or Hodgkin's disease. The present sequence represents the alpha  
 helical region PspA molecule from the EF3296 strain of Streptococcus  
 pneumoniae.

Sequence 416 AA;

Query Match 93.4%; Score 484; DB 8; Length 416;  
 Best Local Similarity 95.2%; Pred. No. 4.5e-35;  
 Matches 99; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 LAKKQTELEKLDNDPBGKTODELDKEAAEAELDKKADLPNKVADLEKEISNLEILLG 60  
 DB 241 LAKKQTELEKLDNDPBGKTODELDKEAAEAELDKKADLPNKVADLEKEISNLEILLG 300

QY 61 GADPEDDTAALPNKLTATKKAELKTKQKELDAALNLELGPDDDEE 104  
 DB 301 GADPEDDTAALPNKLTATKKAELKTKQKELDAALNLELGPDDDEE 344

RESULT 5  
 ADK52497  
 ID ADK52497 standard; protein; 526 AA.

ADK52497;

20-MAY-2004 (first entry)

PspA molecule from the EF3296 strain of Streptococcus pneumoniae.

Streptococcus pneumoniae infection; pneumococcal surface protein A; PspA;  
 hemolytic anemia disease; leukemia; lymphoma; sickle cell anemia;  
 Hodgkin's disease.

Streptococcus pneumoniae.

WO2004016231-A2.

26-FEB-2004.

17-FEB-2003; 2003WO-US008199.

15-MAR-2002; 2002US-0365351P.

(UABR-) UAB RES FOUND.

Briles DE;

WPI; 2004-192068/18.

Treating Streptococcus pneumoniae infection in a subject lacking a  
 functional spleen comprises administering an antibody that recognizes  
 pneumococcal surface protein A (PspA) or its binding portion.

Claim 17; SEQ ID NO 3; 41pp; English.

The present invention relates to treating Streptococcus pneumoniae  
 infection in a subject lacking a functional spleen comprises  
 administering an antibody that recognizes pneumococcal surface protein A  
 (PspA) or its binding portion. The method is useful for treating or  
 preventing Streptococcus pneumoniae infection in a subject lacking a  
 functional spleen. The disease-associated injury is especially due to  
 hemolytic anemia disease, leukemia or lymphoma, especially sickle cell  
 anemia or Hodgkin's disease. The present sequence represents PspA  
 molecule from the EF3296 strain of Streptococcus pneumoniae.

Sequence 526 AA;

Query Match 93.4%; Score 484; DB 8; Length 526;  
 Best Local Similarity 95.2%; Pred. No. 5.9e-35;  
 Matches 99; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 LAKKQTELEKLDNDPBGKTODELDKEAAEAELDKKADLPNKVADLEKEISNLEILLG 60  
 DB 346 LAKKQTELEKLDNDPBGKTODELDKEAAEAELDKKADLPNKVADLEKEISNLEILLG 405

QY 61 GADPEDDTAALPNKLTATKKAELKTKQKELDAALNLELGPDDDEE 104  
 DB 406 GADPEDDTAALPNKLTATKKAELKTKQKELDAALNLELGPDDDEE 449

RESULT 6  
 ABU00449  
 ID ABU00449 standard; protein; 744 AA.

ABU00449;

23-OCT-2003 (revised)

11-FEB-2003 (first entry)

S. pneumoniae type 4 strain protein from coding region #16.



KM antibacterial; antiinflammatory; meningitis; infection; diagnosis;  
KM pneumococcal disease.  
XX  
OS Streptococcus pneumoniae.  
XX  
PN WO200006737-A2.  
XX  
PD 10-FEB-2000.  
XX  
PF 27-JUL-1999; 99WO-GB002451.  
XX  
PR 27-JUL-1998; 98GB-00016337.  
PR 19-MAR-1999; 99US-0125164P.  
XX  
PA (MICK-) MICROBIAL TECHNIQS LTD.  
XX  
PI Gilbert CFG, Hanabro PM;  
XX  
DR WPI; 2000-195300/17.  
XX  
PT New Streptococcal protein, useful as a vaccine, for diagnosis of  
PT pneumococcal diseases and for screening agents capable of antagonizing or  
PT inhibiting expression of the protein.  
XX  
PS Claim 2; Page 95; 108pp; English.  
XX  
CC MAY81501 to MAY81679 represent specifically claimed protein sequences  
CC isolated from Streptococcus pneumoniae. AAA05407 to AAA05590 represent  
CC specifically claimed nucleotide sequences isolated from S. pneumoniae.  
CC The sequences have antibacterial and antiinflammatory properties. The  
CC protein sequences, and fragments of them, are useful as immunogens and/or  
CC antigens. The nucleotide sequences can be used in vaccines and in  
CC diagnostic assays. The proteins and nucleotides can be useful for the  
CC detection and diagnosis of S. pneumoniae. The protein sequences are also  
CC useful for screening an agent capable of antagonizing, inhibiting or  
CC interfering with the function or expression of the proteins in which the  
CC agent is useful for treatment or prophylaxis of S. pneumoniae infection  
CC and meningitis. AAA05591 to AAA05614 represent primers used in the  
CC exemplification of the present invention  
XX  
SQ Sequence 745 AA;  
XX  
Query Match 93.4%; Score 484; DB 3; Length 745;  
Best Local Similarity 95.2%; Pred. No. 8.8e-35;  
Matches 99; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
QY 1 LAKKQTELEKLDNLDPEKTDDELDEKAAEALDKKADLPNKVADLEKEISNLEILLG 60  
DB 346 LAKKQTELEKLDNLDPEKTDDELDEKAAEALDKKADLPNKVADLEKEISNLEILLG 405  
QY 61 GADPEDDTAALPNKLTATKKALEKTKDELDAALNLELGPDDDEE 104  
DB 406 GADSEDDTAALQNKLTATKKALEKTKDELDAALNLELGPDDDEE 449  
XX  
RESULT 9  
AAW61217  
ID AAW61217 standard; protein; 641 AA.  
XX  
AC AAW61217;  
XX  
DT 02-OCT-1998 (first entry)  
XX  
DB Streptococcus pneumoniae SP0092 protein.  
XX  
XX Streptococcus pneumoniae; antigen; vaccine; infection; diagnosis;  
KM Streptococcus pneumoniae; antigen; vaccine; infection; diagnosis;  
KM detection; pneumonia; otitis media; meningitis.  
XX  
OS Streptococcus pneumoniae.  
XX  
XX  
XX Key Location/Qualifiers  
FH Misc-difference 306  
FT /label= unknown

FT /note= "encoded by NCR"  
XX  
PN WO9818930-A2.  
XX  
PD 07-MAY-1998.  
XX  
PF 30-OCT-1997; 97WO-US019422.  
XX  
PR 31-OCT-1996; 96US-0029960P.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
PA Kunesh CA, Choi GH, Johnson LS, Hromockyj A;  
XX  
PI WPI; 1998-272224/24.  
XX  
DR N-PSDB; AAV27403.  
XX  
DR Nucleic acid encoding antigenic peptide(s) from Streptococcus pneumoniae  
PT - or their epitope-containing fragments, useful in protective or  
PT therapeutic vaccines, and for diagnosis.  
XX  
PS Claim 11; Page 82; 118pp; English.  
XX  
CC The present sequence represents a protein from Streptococcus pneumoniae.  
CC The nucleic acid sequence encoding the Streptococcus pneumoniae protein  
CC can be useful in vaccines for inducing protective antibodies against  
CC Streptococcus pneumoniae, for treatment or prevention of infection e.g.  
CC pneumonia, otitis media or meningitis. Probes based on the nucleic acid  
CC are used to detect Streptococcus infection (by usual hybridisation or  
CC amplification methods), also for isolating Streptococcus genes or their  
CC allelic variants. The protein can be used similarly to detect specific  
CC antibodies in standard immunoassays, especially for diagnosing or  
CC monitoring infections. Antibodies which bind the protein are used to  
CC detect corresponding antigens, to purify the protein and for passive  
CC immunisation (optionally coupled to a toxin). Vaccines are administered,  
CC e.g. by injection, orally or through the skin, typically at 0.01-1000  
CC (especially 10-300) mu g/ml per dose  
XX  
SQ Sequence 641 AA;  
XX  
Query Match 93.2%; Score 483; DB 2; Length 641;  
Best Local Similarity 95.2%; Pred. No. 9e-35;  
Matches 99; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
QY 1 LAKKQTELEKLDNLDPEKTDDELDEKAAEALDKKADLPNKVADLEKEISNLEILLG 60  
DB 243 LAKKQTELEKLDNLDPEKTDDELDEKAAEALDKKADLPNKVADLEKEISNLEILLG 302  
QY 61 GADPEDDTAALPNKLTATKKALEKTKDELDAALNLELGPDDDEE 104  
DB 303 GADSEDDTAALQNKLTATKKALEKTKDELDAALNLELGPDDDEE 346  
XX  
RESULT 10  
ABP54636  
ID ABP54636 standard; protein; 641 AA.  
XX  
AC ABP54636;  
XX  
DT 04-SEP-2002 (first entry)  
XX  
DB S. pneumoniae SP092 protein sequence SEQ ID NO:160.  
XX  
XX Streptococcus pneumoniae; epitope; vaccine; antigenic protein;  
KM antibacterial; Streptococcal infection; detection.  
XX  
OS Streptococcus pneumoniae.  
XX  
XX US2002061545-A1.  
XX  
XX 23-MAY-2002.  
XX  
XX 22-JAN-2001; 2001US-00765272.  
XX  
XX

XX 30-OCT-1997; 97US-00961083.  
PR (CHOI/) CHOI G H.  
XX (KUNS/) KUNSCH C A.  
PA (BARA/) BARASH S C.  
PA (DILL/) DILLON P J.  
PA (DOUG/) DOUGHERTY B.  
PA (FANN/) FANNON M R.  
PA (ROSE/) ROSEN C A.  
XX  
PI Choi GH, Kunsch CA, Barash SC, Dillon PJ, Dougherty B, Fannon MR,  
PI Rosen CA;  
XX  
XX WPI; 2002-479261/51.  
DR N-PSDB; ABQ64871.  
XX  
PT New Streptococcus pneumoniae antigens, useful for detecting Streptococcus  
PT and for preventing or attenuating disease caused by Streptococcus  
PT infection.  
XX  
XX Claim 11; Page 43; 70pp; English.  
XX  
XX ABQ84792 to ABQ84904 represents nucleic acids which encode the  
CC Streptococcus pneumoniae antigens given in ABP54557 to ABP54669. The S.  
CC pneumoniae antigens have antibacterial activity and can be used in  
CC vaccines. The S. pneumoniae antigens can also be used to prevent or  
CC attenuate a Streptococcal infection in an animal. The polynucleotides  
CC encoding the S. pneumoniae antigens can be used to detect Streptococcus  
CC nucleic acids. ABQ84905 to ABQ85130 represent primers used in the cloning  
CC of S. pneumoniae ORFs (open reading frames) which are used in an example  
CC from the present invention  
XX  
SQ Sequence 641 AA;

Query Match 93.2%; Score 483; DB 5; Length 641;  
Best Local Similarity 95.2%; Pred. No. 9e-35;  
Matches 99; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
QY 1 LAKKQTELEKLDNLDPBGKTODELDKKAFAEILDKKADELPNKVADLEKEISNLEITLLG 60  
DB 243 LAKKQTELEKLDNLDPBGKTODELDKKAFAEILDKKADELPNKVADLEKEISNLEITLLG 302  
QY 61 GADPEDPTAALPNKLTATKKALEKTOKELDAAALNELGPDGDEER 104  
DB 303 GADKEDPTAALQNKLTATKKALEKTOKELDAAALNELGPDGDEER 346

RESULT 11  
ADCA5241  
ID ADC45241 standard; protein; 641 AA.  
XX  
AC ADC45241;  
XX  
DT 18-DEC-2003 (first entry)  
XX  
DE S. pneumoniae antigenic protein SP092.  
XX  
KM Antigen; bacterial infection; vaccine; pneumonia; antibacterial.  
XX  
OS Streptococcus pneumoniae.  
XX  
PN US6573082-B1.  
XX  
PD 03-JUN-2003.  
XX  
PF 28-MAR-2000; 2000US-00536784.  
XX  
PR 31-OCT-1996; 96US-0029960P.  
PR 30-OCT-1997; 97US-00961083.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX

PI Choi GH, Kunsch CA, Barash SC, Dillon PJ, Dougherty B, Fannon MR;  
PI Rosen CA;  
XX  
DR WPI; 2003-764574/72.  
XX  
DR N-PSDB; ADC45240.  
XX  
PT Novel polynucleotide encoding Streptococcus pneumoniae polypeptides  
PT useful for producing vaccines for prevention or attenuation of infection  
PT by Streptococcus pneumoniae.  
XX  
XX Example 1; SEQ ID NO 160; 58pp; English.  
XX  
XX The invention relates to an isolated polynucleotide consisting of a  
CC Streptococcus pneumoniae nucleic acid (appearing as ADC45122 and encoding  
CC SP028) one of 113 disclosed nucleic acids encoding 113 S. pneumoniae  
CC antigens. Also included are making a recombinant vector by inserting the  
CC nucleic acid into a vector, an isolated polynucleotide consisting of at  
CC least 50 or 100 contiguous nucleotides of the SP028 nucleic acid, and a  
CC recombinant host cell comprising the SP028 polynucleotide. The nucleic  
CC acids are useful as DNA vaccine against Streptococcus pneumoniae  
CC infection (e.g. pneumonia). Nucleic acids derived from the S. pneumoniae  
CC antigen nucleic acids are useful as probes for use in diagnostic methods  
CC for detecting S. pneumoniae gene expression. The present sequence  
CC represents an S. pneumoniae antigenic protein.  
XX  
SQ Sequence 641 AA;

Query Match 93.2%; Score 483; DB 7; Length 641;  
Best Local Similarity 95.2%; Pred. No. 9e-35;  
Matches 99; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
QY 1 LAKKQTELEKLDNLDPBGKTODELDKKAFAEILDKKADELPNKVADLEKEISNLEITLLG 60  
DB 243 LAKKQTELEKLDNLDPBGKTODELDKKAFAEILDKKADELPNKVADLEKEISNLEITLLG 302  
QY 61 GADPEDPTAALPNKLTATKKALEKTOKELDAAALNELGPDGDEER 104  
DB 303 GADKEDPTAALQNKLTATKKALEKTOKELDAAALNELGPDGDEER 346

RESULT 12  
ABW02598  
ID ABW02598 standard; protein; 197 AA.  
XX  
AC ABW02598;  
XX  
DT 12-FEB-2004 (first entry)  
XX  
DE Aci22c pneumococcal surface protein A (PspA) central region.  
XX  
KM Pneumococcal surface protein A; PspA; diagnosis; antigenic; vaccine;  
KM immunological; gene therapy; immunostimulant.  
XX  
OS Unidentified.  
XX  
PN US6592876-B1.  
XX  
PD 15-JUL-2003.  
XX  
PF 15-SEP-1995; 95US-00529055.  
XX  
PR 20-APR-1993; 93US-00048896.  
PR 06-JUN-1995; 95US-00465746.  
XX  
PA (UABR-) UAB RES FOUND.  
XX  
PI Briles DR, McDaniel LS, Swiatlo E, Yother J, Brooks-Walter A;  
XX  
XX WPI; 2003-862841/80.  
XX  
PT Immunological composition for obtaining expression products used for  
PT detecting the presence of Streptococcus pneumoniae or its strain,  
PT comprises at least two different full length isolated gene encoding

PT pneumococcal surface protein A.  
 XX  
 PS Example 6; SEQ ID NO 44; 121bp; English.  
 CC The present invention relates to an immunological composition comprising  
 CC at least 2 different full length isolated genes encoding pneumococcal  
 CC surface protein A (PspA) from different groups based on restriction  
 CC fragment polymorphism analysis. The invention is useful for obtaining  
 CC expression products by recombinant techniques to detect, determine,  
 CC isolate or diagnose the presence of Streptococcus pneumoniae or its  
 CC strain. The expression product is useful for preparing antigenic,  
 CC immunological or vaccine compositions, for eliciting antibodies, an  
 CC immunological response (other than or additional to antibodies) or a  
 CC protective response (including antibody or other immunological response  
 CC by administering compositions to a host). The invention is also useful as  
 CC vaccines and in gene therapy. The present sequence is Acl12c pneumococcal  
 CC surface protein A (PspA) central region. This sequence is used in the  
 CC exemplification of the invention  
 XX  
 SQ Sequence 197 AA;

Query Match 92.7%; Score 480; DB 7; Length 197;  
 Best Local Similarity 93.3%; Pred. No. 4.3e-35;  
 Matches 97; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 LAKKOTELKLDNDPBGKTODELDKEAABALDKKADLPKVVADLEKEISNLEILLG 60  
 DB 22 LAKOTELKLDNDPBGKTODELDKEAABALDKKADLPKVVADLEKEISNLEILLG 81  
 QY 61 GADPEDDTAALPNKLTATKKALEKTQKEIDAAALNLEIGPDGDEEE 104  
 DB 82 GADSEDDTAALPNKLTATKKALEKTQKEIDAAALNLEIGPDGDEEE 125

RESULT 13  
 ABM02606  
 ID ABM02606 standard; protein; 233 AA.  
 XX  
 AC ABM02606;  
 XX  
 DT 12-FEB-2004 (first entry)  
 XX  
 DE Efl109c pneumococcal surface protein A (PspA) central region.  
 XX  
 KM Pneumococcal surface protein A; PspA; diagnosis; antigenic; vaccine;  
 KM immunological; gene therapy; immunostimulant.  
 XX  
 OS Unidentified.  
 XX

PH Key Location/Qualifiers  
 FT Misc-difference 1..233  
 FT /note= "Xaa = Unknown amino acid"  
 XX  
 PN US6592876-B1.  
 XX  
 PD 15-JUL-2003.  
 XX  
 PF 15-SEP-1995; 95US-00529055.  
 XX  
 PR 20-APR-1993; 93US-00048896.  
 PR 06-JUN-1995; 95US-00465746.  
 XX  
 PA (UABR-) UAB RES FOUND.  
 PI Briles DE, McDaniel LS, Swiatlo E, Yother J, Brooks-Walter A;  
 XX  
 DR WPI; 2003-862841/80.  
 XX

Immunological composition for obtaining expression products used for  
 PT detecting the presence of Streptococcus pneumoniae or its strain,  
 PT comprising at least two different full length isolated gene encoding  
 PT pneumococcal surface protein A.  
 XX

PS Example 6; SEQ ID NO 52; 121bp; English.  
 XX  
 CC The present invention relates to an immunological composition comprising  
 CC at least 2 different full length isolated genes encoding pneumococcal  
 CC surface protein A (PspA) from different groups based on restriction  
 CC fragment polymorphism analysis. The invention is useful for obtaining  
 CC expression products by recombinant techniques to detect, determine,  
 CC isolate or diagnose the presence of Streptococcus pneumoniae or its  
 CC strain. The expression product is useful for preparing antigenic,  
 CC immunological or vaccine compositions, for eliciting antibodies, an  
 CC immunological response (other than or additional to antibodies) or a  
 CC protective response (including antibody or other immunological response  
 CC by administering compositions to a host). The invention is also useful as  
 CC vaccines and in gene therapy. The present sequence is Efl109c  
 CC pneumococcal surface protein A (PspA) central region. This sequence is  
 CC used in the exemplification of the invention  
 XX  
 SQ Sequence 233 AA;

Query Match 88.6%; Score 459; DB 7; Length 233;  
 Best Local Similarity 90.4%; Pred. No. 3.9e-33;  
 Matches 94; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 LAKKOTELKLDNDPBGKTODELDKEAABALDKKADLPKVVADLEKEISNLEILLG 60  
 DB 53 LAKOTELKLDNDPBGKTODELDKEAABALDKKADLPKVVADLEKEISNLEILLG 112  
 QY 61 GADPEDDTAALPNKLTATKKALEKTQKEIDAAALNLEIGPDGDEEE 104  
 DB 113 GADSEDDTAALPNKLTATKKALEKTQKEIDAAALNLEIGPDGDEEE 156

RESULT 14  
 AAM14564  
 ID AAM14564 standard; protein; 196 AA.  
 XX  
 AC AAM14564;  
 XX  
 DT 17-OCT-2003 (revised)  
 DT 28-OCT-1997 (first entry)  
 XX  
 DE Streptococcus pneumoniae PspA central region.  
 XX  
 KM PspA; pneumococcal surface protein; vaccine; otitis media; meningitis;  
 KM bacteraemia; pneumonia.  
 XX  
 OS Streptococcus pneumoniae; strain Acl122.  
 XX  
 PN WO9709994-A1.  
 XX  
 PD 20-MAR-1997.  
 XX  
 PF 16-SEP-1996; 96WO-US014819.  
 XX  
 PR 15-SEP-1995; 95US-00529055.  
 XX  
 PA (UABR-) UAB RES FOUND.  
 PI Briles DE, McDaniel LS, Swiatlo E, Yother J, Crain MJ;  
 PI Hollingshead S, Tart R, Brooks-Walter A;  
 XX  
 DR WPI; 1997-202002/18.  
 XX

Streptococcus pneumoniae surface protein PspC and truncated PspA - used  
 PT in vaccines for protecting animals against S.pneumoniae infection.  
 XX

Example 6; Fig 13; 296bp; English.

This sequence shows the central portion, including the C-terminus of the  
 CC alpha-helix region and some of the proline-rich region, of pneumococcal  
 CC surface protein A (PspA) of Streptococcus pneumoniae strain Acl122.  
 CC Comparison of the N-terminal and central regions (AAM14533-57 and  
 CC AAM14562-91) of PspA polypeptides from different pneumococcal strains can  
 CC

CC be used to divide the strains into several families based on sequence  
 CC homologies. PspA polypeptides, or fragments of them, can be used in  
 CC vaccines to protect animals against S. pneumoniae infection and hence for  
 CC the prevention of diseases such as otitis media, meningitis, bacteraemia  
 CC and pneumonia. The sequence of the 3' half of the PspA alpha-helical  
 CC region and the immediate 5' tip of the coding sequence are likely to be  
 CC the critical sequences for predicting PspA cross-reactions and vaccine  
 CC composition. (Updated on 17-OCT-2003 to standardise OS field)

XX Sequence 196 AA;

Query Match 88.1%; Score 456.5; DB 2; Length 196;  
 Best Local Similarity 91.3%; Pred. No. 5.4e-33;  
 Matches 95; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

QY 1 LAKKQTELEKLDNLDPEGKTODELDKEAAEALDKKADLPNKVADLEKEISNLEITLG 60  
 ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 22 LAQKPTGLEKLDLSDPGKRYQDELDEKEAGEALDKKADLPNKVADLEKEISNLEITLG 81

QY 61 GADPEDDTAALPNKLATYKAELEKTOKELDNALNELGPDGDEEE 104  
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 82 GADSEDDTAALPNKLATYKAELEKTKELDPAALNELGPDGDEEE 124

RESULT 15  
 AAW14572  
 ID AAW14572 standard; protein; 233 AA.  
 XX

AC AAW14572;

DT 17-OCT-2003 (revised)  
 DT 28-OCT-1997 (first entry)

XX Streptococcus pneumoniae PspA central region.

KW PspA; pneumococcal surface protein; vaccine; otitis media; meningitis;  
 KM bacteraemia; pneumonia.

OS Streptococcus pneumoniae; strain Efs3296.

XX Key Location/Qualifiers

FT Misc-difference 129 /note= "unidentified amino acid"

FT Misc-difference 131 /note= "unidentified amino acid"

XX W09709994-A1.

XX 20-MAR-1997.

XX 16-SEP-1996; 96WO-US014819.

XX 15-SEP-1995; 95US-00529055.

XX (UABR-) UAB RES FOUND.

XX Briles DE, McDaniel LS, Swiatlo B, Yother J, Crain MJ;

PI Hollingshead S, Tart R, Brooks-Walter A;

XX WPI; 1997-202002/18.

XX Streptococcus pneumoniae surface protein PspC and truncated PspA - used  
 PT in vaccines for protecting animals against S.pneumoniae infection.

XX Example 6; Fig 13; 296pp; English.

CC This sequence shows the central portion, including the C-terminus of the  
 CC alpha-helix region and some of the proline-rich region, of pneumococcal  
 CC surface protein A (PspA) of Streptococcus pneumoniae strain Efs3296.

CC Comparison of the N-terminal and central regions (AAW14533-57 and  
 CC AAW14562-91) of PspA polypeptides from different pneumococcal strains can  
 CC be used to divide the strains into several families based on sequence  
 CC homologies. PspA polypeptides, or fragments of them, can be used in

CC vaccines to protect animals against S. pneumoniae infection and hence for  
 CC the prevention of diseases such as otitis media, meningitis, bacteraemia  
 CC and pneumonia. The sequence of the 3' half of the PspA alpha-helical  
 CC region and the immediate 5' tip of the coding sequence are likely to be  
 CC the critical sequences for predicting PspA cross-reactions and vaccine  
 CC composition. (Updated on 17-OCT-2003 to standardise OS field)

XX Sequence 233 AA;

Query Match 87.3%; Score 452; DB 2; Length 233;  
 Best Local Similarity 89.4%; Pred. No. 1.7e-32;  
 Matches 93; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

QY 1 LAKKQTELEKLDNLDPEGKTODELDKEAAEALDKKADLPNKVADLEKEISNLEITLG 60  
 ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 53 LAQKPTGLEKLDLSDPGKRYQDELDEKEAGEALDKKADLPNKVADLEKEISNLEITLG 112

QY 61 GADPEDDTAALPNKLATYKAELEKTOKELDNALNELGPDGDEEE 104  
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 113 GADSEDDTAALPNKLATYKAELEKTKELDPAALNELGPDGDEEE 156

Search completed: November 19, 2004, 22:20:18  
 Job time : 74.9837 secs



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OM protein - protein search, using sw model

Run on: November 19, 2004, 22:06:04 ; Search time 18.813 seconds  
(without alignments)  
366.612 Million cell updates/sec

Title: US-10-674-755-21

Perfect score: 518

Sequence: 1 LAKKQTELEKLDNDPEBK.....TKKELDALNELGPDDEE 104

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

Issued Patents AA:\*  
1: /cgn2\_6/prodata/1/aa/5A COMB.pep:\*  
2: /cgn2\_6/prodata/1/aa/5B COMB.pep:\*  
3: /cgn2\_6/prodata/1/aa/6A COMB.pep:\*  
4: /cgn2\_6/prodata/1/aa/6B COMB.pep:\*  
5: /cgn2\_6/prodata/1/aa/6C COMB.pep:\*  
6: /cgn2\_6/prodata/1/aa/backfilla1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	518	100.0	104	4	US-09-147-875A-21 Sequence 21, Appl
2	512	98.8	104	2	US-08-710-749-20 Sequence 20, Appl
3	508	98.1	213	4	US-08-529-055-47 Sequence 47, Appl
4	508	98.1	8991	4	US-08-714-741-32 Sequence 32, Appl
5	500	96.5	104	2	US-08-710-749-19 Sequence 19, Appl
6	500	96.5	104	4	US-09-147-875A-20 Sequence 20, Appl
7	483	93.2	641	3	US-08-961-083-160 Sequence 160, App
8	483	93.2	641	4	US-09-536-784-160 Sequence 160, App
9	480	92.7	197	4	US-08-529-055-44 Sequence 44, Appl
10	479	92.5	102	2	US-08-710-749-21 Sequence 21, Appl
11	479	92.5	102	4	US-09-147-875A-18 Sequence 18, Appl
12	459	88.6	233	4	US-08-529-055-52 Sequence 52, Appl
13	375	72.4	80	2	US-09-147-875A-19 Sequence 19, Appl
14	375	72.4	80	4	US-09-147-875A-25 Sequence 25, Appl
15	321	62.0	108	2	US-08-710-749-26 Sequence 26, Appl
16	321	62.0	108	4	US-09-147-875A-23 Sequence 23, Appl
17	321	62.0	211	4	US-08-529-055-67 Sequence 67, Appl
18	315	60.8	108	2	US-08-710-749-24 Sequence 24, Appl
19	315	60.8	108	4	US-09-147-875A-25 Sequence 25, Appl
20	315	60.8	232	4	US-08-529-055-70 Sequence 70, Appl
21	315	60.8	458	4	US-08-529-055-73 Sequence 73, Appl
22	313	60.4	108	4	US-09-147-875A-24 Sequence 24, Appl
23	311	60.0	106	4	US-09-147-875A-22 Sequence 22, Appl
24	306	59.1	212	4	US-08-529-055-68 Sequence 68, Appl
25	303	58.5	108	2	US-08-710-749-22 Sequence 22, Appl
26	303	58.5	108	2	US-08-710-749-23 Sequence 23, Appl
27	266	51.4	108	2	US-08-710-749-25 Sequence 25, Appl

28	266	51.4	108	4	US-09-147-875A-26	Sequence 26, Appl
29	259	50.0	185	4	US-08-529-055-69	Sequence 69, Appl
30	192.5	37.2	119	2	US-08-710-749-27	Sequence 27, Appl
31	192.5	37.2	119	4	US-09-147-875A-27	Sequence 27, Appl
32	192.5	37.2	215	4	US-08-529-055-43	Sequence 43, Appl
33	129.5	25.0	550	4	US-09-583-110-4871	Sequence 4871, Ap
34	128	24.7	288	3	US-08-312-949-4	Sequence 4, Appl
35	128	24.7	288	3	US-08-446-201-4	Sequence 4, Appl
36	128	24.7	619	1	US-08-465-746-2	Sequence 2, Appl
37	128	24.7	619	1	US-08-214-164-2	Sequence 2, Appl
38	128	24.7	619	2	US-08-467-852A-3	Sequence 3, Appl
39	128	24.7	619	2	US-08-246-636-2	Sequence 2, Appl
40	128	24.7	619	2	US-08-247-491A-3	Sequence 3, Appl
41	128	24.7	619	2	US-08-319-795-2	Sequence 2, Appl
42	128	24.7	619	2	US-08-468-985-2	Sequence 2, Appl
43	128	24.7	619	3	US-08-312-949-2	Sequence 2, Appl
44	128	24.7	648	1	US-08-072-070-2	Sequence 2, Appl
45	128	24.7	648	1	US-08-469-434-2	Sequence 2, Appl

#### ALIGNMENTS

```
RESULT 1
US-09-147-875A-21
; Sequence 21, Application US/09147875A
; Patent No. 6638516
; GENERAL INFORMATION:
; APPLICANT: BECKER et al.
; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE PROTEINS
; FILE REFERENCE: 454312-2471
; CURRENT APPLICATION NUMBER: US/09/147,875A
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 21
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-147-875A-21

Query Match      100.0%; Score 518; DB 4; Length 104;
Best Local Similarity 100.0%; Pred. No. 6,9e-43;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LAKKQTELEKLDNDPEBKTDDEKAAEALDKKADLPNKVADLEKEISNIEILG 60
      |||
DB      1 LAKKQTELEKLDNDPEBKTDDEKAAEALDKKADLPNKVADLEKEISNIEILG 60
      |||

QY      61 GADPEDDTRALPNKLTATKKALEKTKQKELDAALNELGPDGDEE 104
      |||
DB      61 GADPEDDTRALPNKLTATKKALEKTKQKELDAALNELGPDGDEE 104
      |||

RESULT 2
US-08-710-749-20
; Sequence 20, Application US/08710749
; Patent No. 5955089
; GENERAL INFORMATION:
; APPLICANT: Briles, David E.
; APPLICANT: Hollingshead, Susan
; APPLICANT: Becker, Robert
; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
```

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/710,749  
FILING DATE: 20-SEP-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Frommer, William S.  
REGISTRATION NUMBER: 25,506  
REFERENCE/DOCKET NUMBER: 454312-2074  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 840-3333  
TELEFAX: (212) 840-0712  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 104 amino acids  
TYPE: amino acid  
STRANDEDNESS: n/a  
TOPOLOGY: linear  
MOLECULE TYPE: amino acid  
US-08-710-749-20

Query Match 98.8%; Score 512; DB 2; Length 104;  
Best Local Similarity 99.0%; Pred. No. 2,6e-42;  
Matches 103; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 LAKQTELEKLDNLDPBGKTQDELDKEAAEALDKKADLPNKVADLEKEISNLEILLG 60  
Db 1 LAKQTELEKLDNLDPBGKTQDELDKEAAEALDKKADLPNKVADLEKEISNLEILLG 60  
Oy 61 GADPEDDTAALPNKLTATKAELEKTOKELDALNLELGPDDGEER 104  
Db 61 GADPEDDTAALPNKLTATKAELEKTPKELDALNLELGPDDGEER 104

## RESULT 3

US-08-529-055-47  
Sequence 47, Application US/08529055  
Patent No. 6592876  
GENERAL INFORMATION:  
APPLICANT: Briles, David E.  
APPLICANT: McDaniel, Larry S.  
APPLICANT: Swiatlo, Edwin  
APPLICANT: Yotter, Janet  
APPLICANT: Brooks-Walter, Alexis  
TITLE OF INVENTION: Pneumococcal Genes, Portions  
TITLE OF INVENTION: Theeoff, Expression Products  
TITLE OF INVENTION: Therefrom, and Uses of Such Genes,  
TITLE OF INVENTION: Portions and Products  
NUMBER OF SEQUENCES: 73  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Curtiss, Morris & Safford, P.C.  
STREET: 530 Fifth Avenue  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/529,055  
FILING DATE: 15-SEP-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Frommer, William S.  
REGISTRATION NUMBER: 25,506  
REFERENCE/DOCKET NUMBER: 454312-2400  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 840-3333  
TELEFAX: (212) 840-0712  
INFORMATION FOR SEQ ID NO: 47:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 213 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-529-055-47

Query Match 98.1%; Score 508; DB 4; Length 213;  
Best Local Similarity 98.1%; Pred. No. 1.5e-41;  
Matches 102; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 LAKQTELEKLDNLDPBGKTQDELDKEAAEALDKKADLPNKVADLEKEISNLEILLG 60  
Db 59 LAKQTELEKLDNLDPBGKTQDELDKEAAEALDKKADLPNKVADLEKEISNLEILLG 118  
Oy 61 GADPEDDTAALPNKLTATKAELEKTOKELDALNLELGPDDGEER 104  
Db 119 GADPEDDTAALPNKLTATKAELEKTPKELDALNLELGPDDGEER 162

## RESULT 4

US-08-714-741-32  
Sequence 32, Application US/08714741  
Patent No. 650613  
GENERAL INFORMATION:  
APPLICANT: Briles, David E.  
APPLICANT: McDaniel, Larry S.  
APPLICANT: Swiatlo, Edwin  
APPLICANT: Yotter, Janet  
APPLICANT: Crain, Marilyn J.  
APPLICANT: Hollingshead, Susan  
APPLICANT: Tart, Rebecca  
APPLICANT: Brooks-Walter, Alexis  
TITLE OF INVENTION: PNEUMOCOCCAL GENES, PORTIONS THEREOF,  
TITLE OF INVENTION: EXPRESSION PRODUCTS THEREFROM, AND USES OF SUCH GENES,  
TITLE OF INVENTION: PORTIONS AND PRODUCTS  
NUMBER OF SEQUENCES: 47  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Curtiss, Morris & Safford, P.C.  
STREET: 530 Fifth Avenue  
CITY: New York  
STATE: New York  
COUNTRY: U.S.  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/714,741  
FILING DATE: 16-SEP-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Frommer, Esq., William S.  
REGISTRATION NUMBER: 25,506  
REFERENCE/DOCKET NUMBER: 454312-2460  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 840-3333  
TELEFAX: (212) 840-0712  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8991 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: amino acid  
US-08-714-741-32

Query Match 98.1%; Score 508; DB 4; Length 8991;  
Best Local Similarity 98.1%; Pred. No. 1.4e-39;  
Matches 102; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LAKQTELEKLDNDPEGKTODELDKEAABALDKKADLPNKVADLEKEISNLEILLG 60  
DB 4625 LAKQTELEKLDNDPEGKTODELDKEAABALDKKADLPNKVADLEKEISNLEILLG 4684

QY 61 GADPBDTALPNKLTATKKALEKTKQKELDAALNLEIGPDGDEE 104  
DB 4685 GADPBDTALPNKLTATKKALEKTKPELDALNLEIGPDGDEE 4728

RESULT 5  
US-08-710-749-19  
Sequence 19, Application US/08710749  
Patent No. 5955089

GENERAL INFORMATION:  
APPLICANT: Brillee, David E.  
APPLICANT: Hollingshead, Susan  
APPLICANT: Becker, Robert  
TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Curtis, Morris & Safford  
STREET: 530 Fifth Avenue  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/710,749  
FILING DATE: 20-SEP-1996  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: Frommer, William S.  
REGISTRATION NUMBER: 25,506  
REFERENCE/DOCKET NUMBER: 454312-2074  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 840-3333  
TELEFAX: (212) 840-0712  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 104 amino acids  
TYPE: amino acid  
STRANDEDNESS: n/a  
TOPOLOGY: linear  
MOLECULE TYPE: amino acid

US-08-710-749-19

Query Match 96.5%; Score 500; DB 2; Length 104;  
Best Local Similarity 97.1%; Pred. No. 3.7e-41;  
Matches 101; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LAKQTELEKLDNDPEGKTODELDKEAABALDKKADLPNKVADLEKEISNLEILLG 60  
DB 1 LAKQTELEKLDNDPEGKTODELDKEAABALDKKADLPNKVADLEKEISNLEILLG 60

QY 61 GADPBDTALPNKLTATKKALEKTKQKELDAALNLEIGPDGDEE 104  
DB 61 GADSEBDTALPNKLTATKKALEKTKQKELDAALNLEIGPDGDEE 104

RESULT 6  
US-09-147-875A-20  
Sequence 20, Application US/09147875A  
Patent No. 6638516

GENERAL INFORMATION:  
APPLICANT: BECKER et al.  
TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE PROTEINS  
FILE REFERENCE: 454312-2471  
CURRENT APPLICATION NUMBER: US/09/147,875A  
CURRENT FILING DATE: 1999-05-24  
NUMBER OF SEQ ID NOS: 28  
SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 20

LENGTH: 104

TYPE: PRT

ORGANISM: Streptococcus pneumoniae

US-09-147-875A-20

Query Match 96.5%; Score 500; DB 4; Length 104;  
Best Local Similarity 97.1%; Pred. No. 3.7e-41;  
Matches 101; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LAKQTELEKLDNDPEGKTODELDKEAABALDKKADLPNKVADLEKEISNLEILLG 60  
DB 1 LAKQTELEKLDNDPEGKTODELDKEAABALDKKADLPNKVADLEKEISNLEILLG 60

QY 61 GADPBDTALPNKLTATKKALEKTKQKELDAALNLEIGPDGDEE 104  
DB 61 GADSEBDTALPNKLTATKKALEKTKQKELDAALNLEIGPDGDEE 104

RESULT 7

US-08-961-083-160  
Sequence 160, Application US/08961083  
Patent No. 6159469

GENERAL INFORMATION:  
APPLICANT: Choi et. al.  
TITLE OF INVENTION: Streptococcus pneumoniae Antigenes and Vaccines  
NUMBER OF SEQUENCES: 452  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: Maryland  
COUNTRY: USA  
ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/961,083

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Brookes, A. Anders

REGISTRATION NUMBER: 36,373

REFERENCE/DOCKET NUMBER: PB340P2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (301) 309-8512

TELEFAX: (301) 309-8504

INFORMATION FOR SEQ ID NO: 160:

SEQUENCE CHARACTERISTICS:

LENGTH: 641 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-961-083-160

Query Match 93.2%; Score 483; DB 3; Length 641;  
Best Local Similarity 95.2%; Pred. No. 1.5e-38;  
Matches 99; Conservative 1; Mismatches 4; Indels 0; Gaps 0;



MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/710,749  
FILING DATE: 20-SEP-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Frommer, William S.  
REGISTRATION NUMBER: 25,506  
REFERENCE/DOCKET NUMBER: 454312-2074  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 840-3333  
TELEFAX: (212) 840-0712  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 102 amino acids  
TYPE: amino acid  
STRANDEDNESS: n/a  
TOPOLOGY: linear  
MOLECULE TYPE: amino acid  
US-08-710-749-21

Query Match 92.5%; Score 479; DB 2; Length 102;  
Best Local Similarity 97.1%; Pred. No. 3.8e-39;  
Matches 101; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

Qy 1 LAKQTELEKLDNDPEGKTODELDKEAAEAELDKKADLPNKVADLEKEISNLEILLG 60  
Db 1 LAKQTELEKLDNDPEGKTODELDKE-AAEAELDKKADLPNKVADLEKEISNLEILLG 58  
Qy 61 GADPEDDTAALPNKLTATKKALEKTQKELDAALNELGPDGDEE 104  
Db 59 GADSEDDTAALPNKLTATKKALEKTQKELDAALNELGPDGDEE 102

RESULT 11  
US-09-147-875A-18  
Sequence 18, Application US/09147875A  
Patent No. 6638516  
GENERAL INFORMATION:  
APPLICANT: BECKER et al.  
TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE PROTEINS  
FILE REFERENCE: 454312-2471  
CURRENT APPLICATION NUMBER: US/09/147,875A  
CURRENT FILING DATE: 1999-05-24  
NUMBER OF SEQ ID NOS: 28  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 18  
LENGTH: 102  
TYPE: PRT  
ORGANISM: Streptococcus pneumoniae  
US-09-147-875A-18

Query Match 92.5%; Score 479; DB 4; Length 102;  
Best Local Similarity 97.1%; Pred. No. 3.8e-39;  
Matches 101; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

Qy 1 LAKQTELEKLDNDPEGKTODELDKEAAEAELDKKADLPNKVADLEKEISNLEILLG 60  
Db 1 LAKQTELEKLDNDPEGKTODELDKE-AAEAELDKKADLPNKVADLEKEISNLEILLG 58  
Qy 61 GADPEDDTAALPNKLTATKKALEKTQKELDAALNELGPDGDEE 104  
Db 59 GADSEDDTAALPNKLTATKKALEKTQKELDAALNELGPDGDEE 102

RESULT 12  
US-08-529-055-52  
Sequence 52, Application US/08529055  
Patent No. 6592876  
GENERAL INFORMATION:

APPLICANT: Briles, David E.  
APPLICANT: McDaniel, Larry S.  
APPLICANT: Swiatlo, Edwin  
APPLICANT: Yocher, Janet  
APPLICANT: Brooks-Walter, Alexis  
TITLE OF INVENTION: Pneumococcal Genes, Portions  
TITLE OF INVENTION: Thereof, Expression Products  
TITLE OF INVENTION: Thereof, and Uses of Such Genes,  
Portions and Products  
NUMBER OF SEQUENCES: 73  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Curtis, Morris & Safford, P.C.  
STREET: 530 Fifth Avenue  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/529,055  
FILING DATE: 15-SEP-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Frommer, William S.  
REGISTRATION NUMBER: 25,506  
REFERENCE/DOCKET NUMBER: 454312-2400  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 840-3333  
TELEFAX: (212) 840-0712  
INFORMATION FOR SEQ ID NO: 52:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 233 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-529-055-52

Query Match 88.6%; Score 459; DB 4; Length 233;  
Best Local Similarity 90.4%; Pred. No. 8.9e-37;  
Matches 94; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 1 LAKQTELEKLDNDPEGKTODELDKEAAEAELDKKADLPNKVADLEKEISNLEILLG 60  
Db 53 LAQKPTGLEKLDSDPEGKTODELDKEAGAEELDKKADLPNKVADLEKEISNLEILLG 112  
Qy 61 GADPEDDTAALPNKLTATKKALEKTQKELDAALNELGPDGDEE 104  
Db 113 GADSEDDTAALPNKLTATKKALEKTQKELDAALNELGPDGDEE 156

RESULT 13  
US-08-710-749-18  
Sequence 18, Application US/08710749  
Patent No. 5955089  
GENERAL INFORMATION:  
APPLICANT: Briles, David E.  
APPLICANT: Hollingshead, Susan  
APPLICANT: Becker, Robert  
TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE  
PROTEINS  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Curtis, Morris & Safford  
STREET: 530 Fifth Avenue  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036

```
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/710,749
FILING DATE: 20-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454312-2074
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 80 amino acids
TYPE: amino acid
STRANDEDNESS: n/a
TOPOLOGY: linear
MOLECULE TYPE: amino acid
US-08-710-749-18
```

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Query Match 72.4%; Score 375; DB 2; Length 80;
Best Local Similarity 95.0%; Pred. No. 3e-29;
Matches 76; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
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QY 25 LDKEAAEAEIDDKADELPNKVADLEKEISNLEILLGADPEDDTALPNKLTATKKAELEK 84
DB 1 LDKEAGAEAEIDDKADGIPNKVSDLEKEISNLEILLGADSEDDTALPNKLTATKKAELEK 60
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```
QY 85 TOKELDAALNELGPDGDEEE 104
DB 61 TOKELDAALNELGPDGDEEE 80
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```
RESULT 14
US-09-147-875A-19
Sequence 19, Application US/09147875A
Patent No. 6638516
GENERAL INFORMATION:
APPLICANT: BECKER et al.
TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE PROTEINS
FILE REFERENCE: 454312-2471
CURRENT APPLICATION NUMBER: US/09/147,875A
CURRENT FILING DATE: 1999-05-24
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 19
LENGTH: 80
TYPE: PRT
ORGANISM: Streptococcus pneumoniae
US-09-147-875A-19
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```
Query Match 72.4%; Score 375; DB 4; Length 80;
Best Local Similarity 95.0%; Pred. No. 3e-29;
Matches 76; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 25 LDKEAAEAEIDDKADELPNKVADLEKEISNLEILLGADPEDDTALPNKLTATKKAELEK 84
DB 1 LDKEAGAEAEIDDKADGIPNKVSDLEKEISNLEILLGADSEDDTALPNKLTATKKAELEK 60
```

```
QY 85 TOKELDAALNELGPDGDEEE 104
DB 61 TOKELDAALNELGPDGDEEE 80
```

```
RESULT 15
US-08-710-749-26
Sequence 26, Application US/08710749
Patent No. 5955089
```

```
GENERAL INFORMATION:
APPLICANT: Biles, David E.
APPLICANT: Hollingshead, Susan
APPLICANT: Becker, Robert
TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE
PROTEINS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESSES:
ADDRESSER: Curtis, Morris & Safford
STREET: 530 Fifth Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/710,749
FILING DATE: 20-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454312-2074
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
STRANDEDNESS: n/a
TOPOLOGY: linear
MOLECULE TYPE: amino acid
US-08-710-749-26
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Query Match 62.0%; Score 321; DB 2; Length 108;
Best Local Similarity 65.7%; Pred. No. 6.9e-24;
Matches 71; Conservative 11; Mismatches 22; Indels 4; Gaps 2;
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QY 1 LAKQTELEKLDNLDPGEKTDQDELDKEAAEAEIDDKADELPNKVADLEKEISNLEILLG 60
DB 1 LKAAAELENTLSTLPGEKTDQDELDKEAAEAEILNKVVALPNQVSELBELEKLEDNLK 60
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```
QY 61 GADP---ED-DTALPNKLTATKKAELEKTKQELDAALNELGPDGDEEE 104
DB 61 DASTNNVEDYIKGLBEAIAITKQAELEKTPKEIDAAALNELGPDGDEEE 108
```

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Search completed: November 19, 2004, 22:39:09
Job time : 19.813 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Comugen Ltd.

OM protein - protein search, using sw model

Run on: November 19, 2004, 22:32:07 / Search time 63.3089 Seconds  
(without alignments)  
581.739 Million cell updates/sec

Title: US-10-674-755-21

Perfect score: 518  
Sequence: 1 LAKKQTELEKLDNLDPBEGK.....TQKELDALNELGPDGDEE 104

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1570615 seqs, 354127592 residues

Total number of hits satisfying chosen parameters: 1570615

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Published Applications AA:

1: /cgn2\_6/ptodata/2/pubppa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/2/pubppa/US06\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/2/pubppa/US06\_PUBCOMB.pep:\*  
4: /cgn2\_6/ptodata/2/pubppa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/2/pubppa/US07\_NEW\_PUB.pep:\*  
6: /cgn2\_6/ptodata/2/pubppa/US07\_PUBCOMB.pep:\*  
7: /cgn2\_6/ptodata/2/pubppa/US08\_NEW\_PUB.pep:\*  
8: /cgn2\_6/ptodata/2/pubppa/US08\_PUBCOMB.pep:\*  
9: /cgn2\_6/ptodata/2/pubppa/US09\_PUBCOMB.pep:\*  
10: /cgn2\_6/ptodata/2/pubppa/US09\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/2/pubppa/US09\_NEW\_PUB.pep:\*  
12: /cgn2\_6/ptodata/2/pubppa/US09\_PUBCOMB.pep:\*  
13: /cgn2\_6/ptodata/2/pubppa/US10\_PUBCOMB.pep:\*  
14: /cgn2\_6/ptodata/2/pubppa/US10\_PUBCOMB.pep:\*  
15: /cgn2\_6/ptodata/2/pubppa/US10\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/2/pubppa/US10\_PUBCOMB.pep:\*  
17: /cgn2\_6/ptodata/2/pubppa/US10\_PUBCOMB.pep:\*  
18: /cgn2\_6/ptodata/2/pubppa/US11\_NEW\_PUB.pep:\*  
19: /cgn2\_6/ptodata/2/pubppa/US60\_NEW\_PUB.pep:\*  
20: /cgn2\_6/ptodata/2/pubppa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	518	100.0	104	US-10-674-755-21	Sequence 21, Appl
2	508	98.1	213	US-10-299-636-62	Sequence 62, Appl
3	500	96.5	104	US-10-674-755-20	Sequence 20, Appl
4	484	93.4	744	US-09-769-787-184	Sequence 184, App
5	483	93.2	641	US-09-765-272-160	Sequence 160, App
6	480	92.7	197	US-10-299-636-59	Sequence 59, Appl
7	479	92.5	102	US-10-674-755-18	Sequence 18, Appl
8	459	88.6	233	US-10-299-636-67	Sequence 67, Appl
9	375	72.4	80	US-10-674-755-19	Sequence 19, Appl
10	321	62.0	108	US-10-674-755-23	Sequence 23, Appl
11	321	62.0	211	US-10-299-636-82	Sequence 82, Appl
12	315	60.8	108	US-10-674-755-25	Sequence 25, Appl
13	315	60.8	232	US-10-299-636-85	Sequence 85, Appl

14	315	60.8	275	16	US-10-414-532-1	Sequence 1, Appl
15	315	60.8	458	15 <td>US-10-299-636-88</td> <td>Sequence 88, Appl</td>	US-10-299-636-88	Sequence 88, Appl
16	315	60.8	653	16 <td>US-10-414-532-26</td> <td>Sequence 26, Appl</td>	US-10-414-532-26	Sequence 26, Appl
17	313	60.0	108	15 <td>US-10-674-755-24</td> <td>Sequence 24, Appl</td>	US-10-674-755-24	Sequence 24, Appl
18	311	60.0	106	15 <td>US-10-674-755-22</td> <td>Sequence 22, Appl</td>	US-10-674-755-22	Sequence 22, Appl
19	306	59.1	212	15 <td>US-10-299-636-83</td> <td>Sequence 83, Appl</td>	US-10-299-636-83	Sequence 83, Appl
20	277	53.5	459	17 <td>US-10-702-305A-18</td> <td>Sequence 18, Appl</td>	US-10-702-305A-18	Sequence 18, Appl
21	266	51.4	108	15 <td>US-10-674-755-25</td> <td>Sequence 25, Appl</td>	US-10-674-755-25	Sequence 25, Appl
22	259	50.0	185	15 <td>US-10-299-636-84</td> <td>Sequence 84, Appl</td>	US-10-299-636-84	Sequence 84, Appl
23	199.5	38.5	487	16 <td>US-10-414-532-34</td> <td>Sequence 34, Appl</td>	US-10-414-532-34	Sequence 34, Appl
24	199.5	38.5	524	16 <td>US-10-414-532-21</td> <td>Sequence 21, Appl</td>	US-10-414-532-21	Sequence 21, Appl
25	199.5	38.5	524	16 <td>US-10-414-532-28</td> <td>Sequence 28, Appl</td>	US-10-414-532-28	Sequence 28, Appl
26	192.5	37.2	119	15 <td>US-10-674-755-27</td> <td>Sequence 27, Appl</td>	US-10-674-755-27	Sequence 27, Appl
27	192.5	37.2	215	15 <td>US-10-299-636-58</td> <td>Sequence 58, Appl</td>	US-10-299-636-58	Sequence 58, Appl
28	187.5	36.2	290	16 <td>US-10-414-532-65</td> <td>Sequence 65, Appl</td>	US-10-414-532-65	Sequence 65, Appl
29	183	35.3	230	16 <td>US-10-414-532-32</td> <td>Sequence 32, Appl</td>	US-10-414-532-32	Sequence 32, Appl
30	183	35.3	350	16 <td>US-10-414-532-19</td> <td>Sequence 19, Appl</td>	US-10-414-532-19	Sequence 19, Appl
31	183	35.3	354	15 <td>US-10-299-636-105</td> <td>Sequence 105, Appl</td>	US-10-299-636-105	Sequence 105, Appl
32	128	24.7	588	15 <td>US-10-299-636-96</td> <td>Sequence 96, Appl</td>	US-10-299-636-96	Sequence 96, Appl
33	128	24.7	619	10 <td>US-09-882-774-1</td> <td>Sequence 1, Appl</td>	US-09-882-774-1	Sequence 1, Appl
34	128	24.7	619	15 <td>US-10-282-122A-73702</td> <td>Sequence 73702, A</td>	US-10-282-122A-73702	Sequence 73702, A
35	128	24.7	619	16 <td>US-10-414-532-72</td> <td>Sequence 72, Appl</td>	US-10-414-532-72	Sequence 72, Appl
36	127	24.5	141	14 <td>US-10-254-995-2</td> <td>Sequence 2, Appl</td>	US-10-254-995-2	Sequence 2, Appl
37	127	24.5	589	9 <td>US-09-748-875-14</td> <td>Sequence 14, Appl</td>	US-09-748-875-14	Sequence 14, Appl
38	127	24.5	589	10 <td>US-09-298-523B-14</td> <td>Sequence 14, Appl</td>	US-09-298-523B-14	Sequence 14, Appl
39	127	24.5	589	15 <td>US-10-299-636-97</td> <td>Sequence 97, Appl</td>	US-10-299-636-97	Sequence 97, Appl
40	127	24.5	643	15 <td>US-10-299-636-95</td> <td>Sequence 95, Appl</td>	US-10-299-636-95	Sequence 95, Appl
41	127	24.5	670	9 <td>US-09-748-875-63</td> <td>Sequence 63, Appl</td>	US-09-748-875-63	Sequence 63, Appl
42	127	24.5	670	10 <td>US-09-298-523B-63</td> <td>Sequence 63, Appl</td>	US-09-298-523B-63	Sequence 63, Appl
43	127	24.5	690	9 <td>US-09-748-875-61</td> <td>Sequence 61, Appl</td>	US-09-748-875-61	Sequence 61, Appl
44	127	24.5	690	10 <td>US-09-298-523B-61</td> <td>Sequence 61, Appl</td>	US-09-298-523B-61	Sequence 61, Appl
45	127	24.5	691	9 <td>US-09-748-875-1</td> <td>Sequence 1, Appl</td>	US-09-748-875-1	Sequence 1, Appl

#### ALIGNMENTS

RESULT 1  
US-10-674-755-21  
Sequence 21, Application US/10674755  
Publication No. US20040067237A1  
GENERAL INFORMATION:  
APPLICANT: BECKER et al.  
TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE PROTEINS  
FILE REFERENCE: 454312-2471  
CURRENT APPLICATION NUMBER: US/10/674,755  
CURRENT FILING DATE: 2003-09-30  
PRIOR APPLICATION NUMBER: US/09/147,875A  
PRIOR FILING DATE: 1999-05-24  
NUMBER OF SEQ ID NOS: 28  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 21  
LENGTH: 104  
TYPE: PRT  
ORGANISM: Streptococcus pneumoniae  
US-10-674-755-21

Query Match 100.0%, Score 518, DB 15, Length 104;  
Best local similarity 100.0%, Pred. No. 1,3e-36;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LAKKQTELEKLDNLDPBEGKTODEIDKEAAEELDKKADELPNKVADELKEISNLEILG 60  
DB 1 LAKKQTELEKLDNLDPBEGKTODEIDKEAAEELDKKADELPNKVADELKEISNLEILG 60  
QY 61 GADPEDTPALPNKATTKAELEKTQKELDALNELGPDGDEE 104  
DB 61 GADPEDTPALPNKATTKAELEKTQKELDALNELGPDGDEE 104  
RESULT 2  
US-10-299-636-62  
Sequence 62, Application US/10299636

```
; Publication No. US20040077847A1
; GENERAL INFORMATION:
; APPLICANT: Briles, David E
; APPLICANT: McDaniel, Larry S
; APPLICANT: Swatilo, Edwin
; APPLICANT: Yoche, Janet
; APPLICANT: Craign, Marilyn J
; APPLICANT: Hollingshead, Susan
; APPLICANT: Tart, Rebecca
; APPLICANT: Brooke-Walter, Alexis
; TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEINS AND USES THEREOF
; FILE REFERENCE: 57909/361
; CURRENT APPLICATION NUMBER: US/10/299,636
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: 06/714,741
; PRIOR FILING DATE: 1996-09-16
; PRIOR APPLICATION NUMBER: 08/529,055
; PRIOR FILING DATE: 1995-09-15
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 62
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (2)
; OTHER INFORMATION: Xaa at position 2 is unknown
US-10-299-636-62
```

```
Query Match          98.1%; Score 508; DB 15; Length 213;
Best Local Similarity 98.1%; Pred. No. 2.1e-35;
Matches 102; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      1 LAKKQTELEKLDNDPEGKTQDELDKAAEAELDKKADELPNKVADLEKEISNLEILLG 60
Db      59 LAKKQTELEKLDNDPEGKTQDELDKAAEAELDKKADELPNKVADLEKEISNLEILLG 118
```

```
Qy      61 GADBEDDTAALPNKLTATKKALEKTQKELDAALNELGPDGDEE 104
Db      119 GADBEDDTAALPNKLTATKKALEKTQKELDAALNELGPDGDEE 162
```

```
RESULT 3
US-10-674-755-20
; Sequence 20, Application US/10674755
; Publication No. US20040067237A1
; GENERAL INFORMATION:
; APPLICANT: BECKER et al.
; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE PROTEINS
; FILE REFERENCE: 454312-2471
; CURRENT APPLICATION NUMBER: US/10/674,755
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: US/09/147,875A
; PRIOR FILING DATE: 1999-05-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-674-755-20
```

```
Query Match          96.5%; Score 500; DB 15; Length 104;
Best Local Similarity 97.1%; Pred. No. 4.3e-35;
Matches 101; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      1 LAKKQTELEKLDNDPEGKTQDELDKAAEAELDKKADELPNKVADLEKEISNLEILLG 60
Db      1 LAKKQTELEKLDNDPEGKTQDELDKAAEAELDKKADELPNKVADLEKEISNLEILLG 60
Qy      61 GADBEDDTAALPNKLTATKKALEKTQKELDAALNELGPDGDEE 104
```

```
Db      61 GADBEDDTAALPNKLTATKKALEKTQKELDAALNELGPDGDEE 104
RESULT 4
US-09-769-787-184
; Sequence 184, Application US/09769787
; Publication No. US20030091577A1
; GENERAL INFORMATION:
; APPLICANT: Microbial Technics Limited
; APPLICANT: Gilbert, Christophe FG
; APPLICANT: Hansbro, Philip M
; TITLE OF INVENTION: Proteins
; FILE REFERENCE: PWC/P21129WO
; CURRENT APPLICATION NUMBER: US/09/769,787
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: GB 9816337.1
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: US 60/125164
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 388
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 184
; LENGTH: 744
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-769-787-184
```

```
Query Match          93.4%; Score 484; DB 10; Length 744;
Best Local Similarity 95.2%; Pred. No. 9.8e-33;
Matches 99; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy      1 LAKKQTELEKLDNDPEGKTQDELDKAAEAELDKKADELPNKVADLEKEISNLEILLG 60
Db      346 LAKKQTELEKLDNDPEGKTQDELDKAAEAELDKKADELPNKVADLEKEISNLEILLG 405
```

```
Qy      61 GADBEDDTAALPNKLTATKKALEKTQKELDAALNELGPDGDEE 104
Db      406 GADBEDDTAALPNKLTATKKALEKTQKELDAALNELGPDGDEE 449
```

```
RESULT 5
US-09-765-272-160
; Sequence 160, Application US/09765272
; Patent No. US20020061545A1
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/765,272
; FILING DATE: 22-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/961,083
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
```



TELEFAX: (301) 309-8512  
INFORMATION FOR SEQ ID NO: 160:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 641 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 160:  
US-09-765-272-160

Query Match 93.2%; Score 483; DB 9; Length 641;  
Best Local Similarity 95.2%; Pred. No. 1e-32;  
Matches 99; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 LAKKOTELKLDNDLDPGKTODELDKKAABALDKKADLPNKVADLEKEISNLEILLG 60  
DB 243 LAKKOTELKLDLSDLPBGKTODELDKKAABALDKKADLPNKVADLEKEISNLEILLG 302  
QY 61 GADPEDDTAALPNKLTATKKALEKTOKELDAALNLEIGPDGDEE 104  
DB 303 GADPEDDTAALPNKLTATKKALEKTOKELDAALNLEIGPDGDEE 346

## RESULT 6

US-10-299-636-59  
Sequence 59, Application US/10299636  
Publication No. US20040077847A1

GENERAL INFORMATION:  
APPLICANT: Briles, David B  
APPLICANT: McDaniel, Larry S  
APPLICANT: Swiatlo, Edwin  
APPLICANT: Yother, Janet  
APPLICANT: Crain, Marilyn J  
APPLICANT: Hollingshead, Susan  
APPLICANT: Tart, Rebecca  
APPLICANT: Brooks-Walter, Alexis  
TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEINS AND USES THEREOF  
FILE REFERENCE: 57909/361  
CURRENT APPLICATION NUMBER: US/10/299,636  
CURRENT FILING DATE: 2002-11-19  
PRIOR APPLICATION NUMBER: 08/714,741  
PRIOR FILING DATE: 1996-09-16  
PRIOR APPLICATION NUMBER: 08/529,055  
PRIOR FILING DATE: 1995-09-15  
NUMBER OF SEQ ID NOS: 111  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 59  
LENGTH: 197  
TYPE: prt  
ORGANISM: Streptococcus pneumoniae  
US-10-299-636-59

Query Match 92.7%; Score 480; DB 15; Length 197;  
Best Local Similarity 93.3%; Pred. No. 4.5e-33;  
Matches 97; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 LAKKOTELKLDNDLDPGKTODELDKKAABALDKKADLPNKVADLEKEISNLEILLG 60  
DB 22 LAQKOTELKLDLSDLPBGKTODELDKKAABALDKKADLPNKVADLEKEISNLEILLG 81  
QY 61 GADPEDDTAALPNKLTATKKALEKTOKELDAALNLEIGPDGDEE 104  
DB 82 GADPEDDTAALPNKLTATKKALEKTOKELDAALNLEIGPDGDEE 125

## RESULT 7

US-10-674-755-18  
Sequence 18, Application US/10674755  
Publication No. US20040067237A1

GENERAL INFORMATION:  
APPLICANT: BECKER et al.  
TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE PROTEINS

FILE REFERENCE: 454312-2471  
CURRENT APPLICATION NUMBER: US/10/674,755  
CURRENT FILING DATE: 2003-09-30  
PRIOR APPLICATION NUMBER: US/09/147,875A  
PRIOR FILING DATE: 1999-05-24  
NUMBER OF SEQ ID NOS: 28  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 18  
LENGTH: 102  
TYPE: prt  
ORGANISM: Streptococcus pneumoniae  
US-10-674-755-18

Query Match 92.5%; Score 479; DB 15; Length 102;  
Best Local Similarity 97.1%; Pred. No. 2.5e-31;  
Matches 101; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

QY 1 LAKKOTELKLDNDLDPGKTODELDKKAABALDKKADLPNKVADLEKEISNLEILLG 60  
DB 1 LAKKOTELKLDLSDLPBGKTODELDKKAABALDKKADLPNKVADLEKEISNLEILLG 58  
QY 61 GADPEDDTAALPNKLTATKKALEKTOKELDAALNLEIGPDGDEE 104  
DB 59 GADPEDDTAALPNKLTATKKALEKTOKELDAALNLEIGPDGDEE 102

## RESULT 8

US-10-299-636-67  
Sequence 67, Application US/10299636  
Publication No. US20040077847A1

GENERAL INFORMATION:  
APPLICANT: Briles, David B  
APPLICANT: McDaniel, Larry S  
APPLICANT: Swiatlo, Edwin  
APPLICANT: Yother, Janet  
APPLICANT: Crain, Marilyn J  
APPLICANT: Hollingshead, Susan  
APPLICANT: Tart, Rebecca  
APPLICANT: Brooks-Walter, Alexis  
TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEINS AND USES THEREOF  
FILE REFERENCE: 57909/361  
CURRENT APPLICATION NUMBER: US/10/299,636  
CURRENT FILING DATE: 2002-11-19  
PRIOR APPLICATION NUMBER: 08/714,741  
PRIOR FILING DATE: 1996-09-16  
PRIOR APPLICATION NUMBER: 08/529,055  
PRIOR FILING DATE: 1995-09-15  
NUMBER OF SEQ ID NOS: 111  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 67  
LENGTH: 233  
TYPE: prt  
ORGANISM: Streptococcus pneumoniae

FEATURE:  
NAME/KEY: UNSURE  
LOCATION: (129)  
OTHER INFORMATION: Xaa at position 129 is unknown  
NAME/KEY: UNSURE  
LOCATION: (131)  
OTHER INFORMATION: Xaa at position 131 is unknown  
US-10-299-636-67

Query Match 88.6%; Score 459; DB 15; Length 233;  
Best Local Similarity 90.4%; Pred. No. 3.3e-31;  
Matches 94; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 LAKKOTELKLDNDLDPGKTODELDKKAABALDKKADLPNKVADLEKEISNLEILLG 60  
DB 53 LAQKOTELKLDLSDLPBGKTODELDKKAABALDKKADLPNKVADLEKEISNLEILLG 112  
QY 61 GADPEDDTAALPNKLTATKKALEKTOKELDAALNLEIGPDGDEE 104

Db 113 GAU5EDDTAALPNKLAAXKAELEKTOKELDAAAPNELGPDGDEER 156

RESULT 9

US-10-674-755-19

Sequence 19, Application US/10674755

Publication No. US20040067237A1

GENERAL INFORMATION:

APPLICANT: BECKER et al.

TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE PROTEINS

FILE REFERENCE: 454312-2471

CURRENT APPLICATION NUMBER: US/10/674,755

CURRENT FILING DATE: 2003-09-30

PRIOR APPLICATION NUMBER: US/09/147,875A

PRIOR FILING DATE: 1999-05-24

NUMBER OF SEQ ID NOS: 28

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 19

LENGTH: 80

TYPE: PRT

ORGANISM: Streptococcus pneumoniae

US-10-674-755-19

Query Match 72.4%; Score 375; DB 15; Length 80;

Best Local Similarity 95.0%; Pred. No. 1.3e-24;

Matches 76; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 25 LDKKAAAELEKLDNLPDEGKTODELDKKAAPAELELDKKADELPNKVADLEKEISNLEILG 84

DB 1 LDKKAGAELELDKADGDPNKVSDLEKEISNLEILGGAU5EDDTAALPNKLAATKKAELK 60

QY 85 TOKELDAALNELGPDGDEER 104

DB 61 TOKELDAALNELGPDGDEER 80

RESULT 10

US-10-674-755-23

Sequence 23, Application US/10674755

Publication No. US20040067237A1

GENERAL INFORMATION:

APPLICANT: BECKER et al.

TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE PROTEINS

FILE REFERENCE: 454312-2471

CURRENT APPLICATION NUMBER: US/10/674,755

CURRENT FILING DATE: 2003-09-30

PRIOR APPLICATION NUMBER: US/09/147,875A

PRIOR FILING DATE: 1999-05-24

NUMBER OF SEQ ID NOS: 28

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 23

LENGTH: 108

TYPE: PRT

ORGANISM: Streptococcus pneumoniae

US-10-674-755-23

Query Match 62.0%; Score 321; DB 15; Length 108;

Best Local Similarity 65.7%; Pred. No. 6.9e-20;

Matches 71; Conservative 11; Mismatches 22; Indels 4; Gaps 2;

QY 1 LAKKQTELEKLDNLPDEGKTODELDKKAAPAELELDKKADELPNKVADLEKEISNLEILG 60

DB 1 LKKAABALELNLSTLDPGKTODELDKKAAPAELELNKVEALPNQVSELEBELSKLEEDNLK 60

QY 61 GADP---ED-DTAAALPNKLAATKKALEKTOKELDAAALNELGPDGDEER 104

DB 61 DAETNNVEDYIKGELBEAIAITKQALEKTPKELDAALNELGPDGDEER 108

RESULT 11

US-10-299-636-82

Sequence 82, Application US/10299636

Publication No. US2004007847A1

GENERAL INFORMATION:

APPLICANT: Briles, David E

APPLICANT: McDaniel, Larry S

APPLICANT: Swiatlo, Edwin

APPLICANT: Yocher, Janet

APPLICANT: Crain, Marilyn J

APPLICANT: Hollingshead, Susan

APPLICANT: Tarr, Rebecca

APPLICANT: Brooks-Walter, Alexis

TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEINS AND USES THEREOF

FILE REFERENCE: 57909/361

CURRENT APPLICATION NUMBER: US/10/299,636

CURRENT FILING DATE: 2002-11-19

PRIOR APPLICATION NUMBER: 08/714,741

PRIOR FILING DATE: 1996-09-16

PRIOR APPLICATION NUMBER: 08/529,055

PRIOR FILING DATE: 1995-09-15

NUMBER OF SEQ ID NOS: 111

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 82

LENGTH: 211

TYPE: PRT

ORGANISM: Streptococcus pneumoniae

US-10-299-636-82

Query Match 62.0%; Score 321; DB 15; Length 211;

Best Local Similarity 65.7%; Pred. No. 1.5e-19;

Matches 71; Conservative 11; Mismatches 22; Indels 4; Gaps 2;

QY 1 LAKKQTELEKLDNLPDEGKTODELDKKAAPAELELDKKADELPNKVADLEKEISNLEILG 60

DB 25 LKKAABALELNLSTLDPGKTODELDKKAAPAELELNKVEALPNQVSELEBELSKLEEDNLK 84

QY 61 GADP---ED-DTAAALPNKLAATKKALEKTOKELDAAALNELGPDGDEER 104

DB 85 DAETNNVEDYIKGELBEAIAITKQALEKTPKELDAALNELGPDGDEER 132

RESULT 12

US-10-674-755-25

Sequence 25, Application US/10674755

Publication No. US20040067237A1

GENERAL INFORMATION:

APPLICANT: BECKER et al.

TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE PROTEINS

FILE REFERENCE: 454312-2471

CURRENT APPLICATION NUMBER: US/10/674,755

CURRENT FILING DATE: 2003-09-30

PRIOR APPLICATION NUMBER: US/09/147,875A

PRIOR FILING DATE: 1999-05-24

NUMBER OF SEQ ID NOS: 28

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 25

LENGTH: 108

TYPE: PRT

ORGANISM: Streptococcus pneumoniae

US-10-674-755-25

Query Match 60.8%; Score 315; DB 15; Length 108;

Best Local Similarity 65.7%; Pred. No. 2.2e-19;

Matches 71; Conservative 11; Mismatches 22; Indels 4; Gaps 2;

QY 1 LAKKQTELEKLDNLPDEGKTODELDKKAAPAELELDKKADELPNKVADLEKEISNLEILG 60

DB 1 LEDAELELEKVLATLDPGKTODELDKKAAPAELELNKVEALPNQVSELEBELSKLEEDNLK 60

QY 61 GADP---ED-DTAAALPNKLAATKKALEKTOKELDAAALNELGPDGDEER 104

DB 61 DAETNNVEDYIKGELBEAIAITKKALEKTOKELDAAALNELGPDGDEER 108

RESULT 13

US-10-299-636-85

; Sequence 85, Application US/10299636  
; Publication No. US2004007847A1  
; GENERAL INFORMATION:  
; APPLICANT: Briles, David E  
; APPLICANT: McDaniel, Larry S  
; APPLICANT: Swiatlo, Edwin  
; APPLICANT: Yotter, Janet  
; APPLICANT: Crain, Marilyn J  
; APPLICANT: Hollingshead, Susan  
; APPLICANT: Tarr, Rebecca  
; APPLICANT: Brooks-Walter, Alexis  
; TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEINS AND USES THEREOF  
; FILE REFERENCE: 57909/361  
; CURRENT FILING DATE: 2002-11-19  
; PRIOR APPLICATION NUMBER: US/10/299,636  
; PRIOR FILING DATE: 1996-09-16  
; PRIOR APPLICATION NUMBER: 08/529,055  
; PRIOR FILING DATE: 1995-09-15  
; NUMBER OF SEQ ID NOS: 111  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 85  
; LENGTH: 232  
; TYPE: PRT  
; ORGANISM: Streptococcus pneumoniae  
US-10-299-636-85

Query Match 60.8%; Score 315; DB 15; Length 232;  
Best Local Similarity 65.7%; Pred. No. 5.5e-19;  
Matches 71; Conservative 11; Mismatches 22; Indels 4; Gaps 2;

Qy 1 LAKKQTELEKLDNDPPEKGTODELDKEAAEALDKKADELPNKVADLEKEISNLEILG 60  
Db 51 LEDALELEKVLATIDPEKGTODELDKEAAEALNEKVEALONQVALEEBELSKLEDNIK 110  
61 GADP---ED-DTAAIPNKLATKKALEKTKQKELDAALNELGPDGDEE 104  
Db 111 DAEITNVVDYIKKGLBAIATKKALEKTKQKELDAALNELGPDGDEE 158

RESULT 14  
US-10-414-532-1  
; Sequence 1, Application US/10414532  
; Publication No. US20040101531A1  
; GENERAL INFORMATION:  
; APPLICANT: KANG, HO YOUNG  
; APPLICANT: CURTIS, III, ROY  
; TITLE OF INVENTION: IMPROVED IMMUNOGENIC COMPOSITIONS AND VACCINES COMPRISING  
; TITLE OF INVENTION: CARRIER BACTERIA THAT SECRETE ANTIGENS  
; FILE REFERENCE: 56029-40437  
; CURRENT APPLICATION NUMBER: US/10/414,532  
; CURRENT FILING DATE: 2003-04-15  
; PRIOR APPLICATION NUMBER: 60/372,710  
; PRIOR FILING DATE: 2002-04-16  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 1  
; LENGTH: 275  
; TYPE: PRT  
; ORGANISM: Streptococcus pneumoniae  
US-10-414-532-1

Query Match 60.8%; Score 315; DB 16; Length 275;  
Best Local Similarity 65.7%; Pred. No. 6.7e-19;  
Matches 71; Conservative 11; Mismatches 22; Indels 4; Gaps 2;

Qy 1 LAKKQTELEKLDNDPPEKGTODELDKEAAEALDKKADELPNKVADLEKEISNLEILG 60  
Db 167 LEDALELEKVLATIDPEKGTODELDKEAAEALNEKVEALONQVALEEBELSKLEDNIK 226  
61 GADP---ED-DTAAIPNKLATKKALEKTKQKELDAALNELGPDGDEE 104  
Db 227 DAEITNVVDYIKKGLBAIATKKALEKTKQKELDAALNELGPDGDEE 274

RESULT 15  
US-10-299-636-88  
; Sequence 88, Application US/10299636  
; Publication No. US2004007847A1  
; GENERAL INFORMATION:  
; APPLICANT: Briles, David E  
; APPLICANT: McDaniel, Larry S  
; APPLICANT: Swiatlo, Edwin  
; APPLICANT: Yotter, Janet  
; APPLICANT: Crain, Marilyn J  
; APPLICANT: Hollingshead, Susan  
; APPLICANT: Tarr, Rebecca  
; APPLICANT: Brooks-Walter, Alexis  
; TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEINS AND USES THEREOF  
; FILE REFERENCE: 57909/361  
; CURRENT APPLICATION NUMBER: US/10/299,636  
; CURRENT FILING DATE: 2002-11-19  
; PRIOR APPLICATION NUMBER: 08/714,741  
; PRIOR FILING DATE: 1996-09-16  
; PRIOR APPLICATION NUMBER: 08/529,055  
; PRIOR FILING DATE: 1995-09-15  
; NUMBER OF SEQ ID NOS: 111  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 88  
; LENGTH: 458  
; TYPE: PRT  
; ORGANISM: Streptococcus pneumoniae  
US-10-299-636-88

Query Match 60.8%; Score 315; DB 15; Length 458;  
Best Local Similarity 65.7%; Pred. No. 1.2e-18;  
Matches 71; Conservative 11; Mismatches 22; Indels 4; Gaps 2;

Qy 1 LAKKQTELEKLDNDPPEKGTODELDKEAAEALDKKADELPNKVADLEKEISNLEILG 60  
Db 276 LEDALELEKVLATIDPEKGTODELDKEAAEALNEKVEALONQVALEEBELSKLEDNIK 335  
61 GADP---ED-DTAAIPNKLATKKALEKTKQKELDAALNELGPDGDEE 104  
Db 336 DAEITNVVDYIKKGLBAIATKKALEKTKQKELDAALNELGPDGDEE 383

Search completed: November 19, 2004, 23:28:07  
Job time : 64.3089 secs

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OM protein - protein search, using sw model

Run on: November 19, 2004, 22:08:34 ; Search time 240.024 Seconds  
(without alignments)  
480.084 Million cell updates/sec

Title: US-10-674-755-21

Perfect score: 518  
Sequence: 1 LAKKQTELEKLDNLDPECK.....TKKELDAALNELGPDDEEE 104

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 6730630 seqs, 1107998698 residues

Total number of hits satisfying chosen parameters: 6730630

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Pending Patents AA Main:\*

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2: /cgn2\_6/ptodata/1/paa/US06\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/paa/US07\_COMB.pep.\*  
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11: /cgn2\_6/ptodata/1/paa/US087\_COMB.pep.\*  
12: /cgn2\_6/ptodata/1/paa/US088\_COMB.pep.\*  
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25: /cgn2\_6/ptodata/1/paa/US099B\_COMB.pep.\*  
26: /cgn2\_6/ptodata/1/paa/US100\_COMB.pep.\*  
27: /cgn2\_6/ptodata/1/paa/US101\_COMB.pep.\*  
28: /cgn2\_6/ptodata/1/paa/US102\_COMB.pep.\*  
29: /cgn2\_6/ptodata/1/paa/US103\_COMB.pep.\*  
30: /cgn2\_6/ptodata/1/paa/US104\_COMB.pep.\*  
31: /cgn2\_6/ptodata/1/paa/US105\_COMB.pep.\*  
32: /cgn2\_6/ptodata/1/paa/US106\_COMB.pep.\*  
33: /cgn2\_6/ptodata/1/paa/US107\_COMB.pep.\*  
34: /cgn2\_6/ptodata/1/paa/US108\_COMB.pep.\*  
35: /cgn2\_6/ptodata/1/paa/US109\_COMB.pep.\*  
36: /cgn2\_6/ptodata/1/paa/US60\_COMB.pep.\*

Prod. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	518	100.0	104	32	US-10-674-755-21	Sequence 21, Appl
2	508	98.1	213	28	US-10-299-636-62	Sequence 62, Appl
3	500	96.5	104	32	US-10-674-755-20	Sequence 20, Appl
4	498	96.1	502	22	US-09-791-537-114569	Sequence 114569,
5	484	93.4	744	1	PCT-US03-27401-251	Sequence 251, App
6	484	93.4	744	22	US-09-765-787-184	Sequence 184, App
7	484	93.4	744	30	US-10-472-928-32	Sequence 32, Appl
8	484	93.4	744	34	US-10-873-528-184	Sequence 184, App
9	484	93.4	744	13	US-08-961-083-160	Sequence 160, App
10	483	93.2	641	13	US-08-961-083-160	Sequence 160, App
11	483	93.2	641	22	US-09-765-271-160	Sequence 160, App
12	483	93.2	641	22	US-09-765-272-160	Sequence 160, App
13	483	93.2	641	22	US-09-765-272A-160	Sequence 160, App
14	480	92.7	107	32	US-10-299-636-59	Sequence 59, Appl
15	479	92.5	102	32	US-10-674-755-18	Sequence 18, Appl
16	459	88.6	233	28	US-10-299-636-67	Sequence 67, Appl
17	375	72.4	80	32	US-10-674-755-19	Sequence 19, Appl
18	322	62.2	479	22	US-09-791-537-114578	Sequence 114578,
19	321	62.0	108	32	US-10-674-755-23	Sequence 23, Appl
20	321	62.0	211	28	US-10-299-636-82	Sequence 82, Appl
21	315	60.8	108	32	US-10-674-755-25	Sequence 25, Appl
22	315	60.8	232	28	US-10-299-636-85	Sequence 85, Appl
23	315	60.8	275	30	US-10-414-532-1	Sequence 1, Appl
24	315	60.8	275	36	US-60-372-710-1	Sequence 1, Appl
25	315	60.8	458	28	US-10-299-636-88	Sequence 88, Appl
26	315	60.8	653	30	US-10-414-532-26	Sequence 26, Appl
27	315	60.8	653	36	US-60-372-710-26	Sequence 26, Appl
28	313	60.4	108	32	US-10-674-755-24	Sequence 24, Appl
29	311	60.0	106	32	US-10-674-755-22	Sequence 22, Appl
30	306	59.1	212	28	US-10-299-636-83	Sequence 83, Appl
31	297	57.3	480	22	US-09-791-537-114577	Sequence 114577,
32	277	53.5	459	1	PCT-US03-35529-18	Sequence 18, Appl
33	277	53.5	459	33	US-10-702-305A-18	Sequence 18, Appl
34	266	51.4	108	32	US-10-674-755-26	Sequence 26, Appl
35	259	50.0	185	28	US-10-299-636-84	Sequence 84, Appl
36	245.5	47.4	456	22	US-09-791-537-114571	Sequence 114571,
37	245.5	47.4	461	22	US-09-791-537-114571	Sequence 114571,
38	199.5	38.5	487	1	PCT-US03-11802-21	Sequence 21, Appl
39	199.5	38.5	487	30	US-10-414-532-34	Sequence 34, Appl
40	199.5	38.5	487	30	US-10-414-532-31	Sequence 31, Appl
41	199.5	38.5	524	30	US-10-414-532-28	Sequence 28, Appl
42	199.5	38.5	524	36	US-60-372-710-28	Sequence 28, Appl
43	192.5	37.2	119	32	US-10-674-755-27	Sequence 27, Appl
44	192.5	37.2	215	28	US-10-299-636-58	Sequence 58, Appl
45	187.5	36.2	290	30	US-10-414-532-65	Sequence 65, Appl

#### ALIGNMENTS

RESULT 1  
US-10-674-755-21  
Sequence 21, Application US/10674755  
GENERAL INFORMATION:  
APPLICANT: BECKER et al.  
TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE PROTEINS  
FILE REFERENCE: 454312-2471  
CURRENT FILING DATE: 2003-09-30  
PRIOR APPLICATION NUMBER: US/09/147,875A  
PRIORITY FILING DATE: 1999-05-24  
NUMBER OF SEQ ID NOS: 28  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 21  
LENGTH: 104  
TYPE: PRT  
ORGANISM: Streptococcus pneumoniae  
US-10-674-755-21

Query Match 100.0% Score 518; DB 32; Length 104;

Best Local Similarity 100.0%; Pred. No. 7.5e-38;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAKKQTELEKLDNLDPBGKTQDELDKKAABAEIDKKADELPNKVADLEKEISNLEITLG 60  
Db 1 LAKKQTELEKLDNLDPBGKTQDELDKKAABAEIDKKADELPNKVADLEKEISNLEITLG 60

QY 61 GADEDDTAALPNKLTATKKALEKTOKELDALNALNELGPDGDEE 104  
Db 61 GADEDDTAALPNKLTATKKALEKTOKELDALNALNELGPDGDEE 104

RESULT 2  
US-10-299-636-62

; Sequence 62, Application US/10299636  
; GENERAL INFORMATION:

; APPLICANT: Briles, David E  
; APPLICANT: McDaniel, Larry S  
; APPLICANT: Swatilo, Edwin  
; APPLICANT: Yochev, Janet  
; APPLICANT: Crahn, Marilyn J  
; APPLICANT: Hollingshead, Susan  
; APPLICANT: Tart, Rebecca  
; APPLICANT: Brooks-Walter, Alexis  
; TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEINS AND USES THEREOF  
; FILE REFERENCE: 57909/361  
; CURRENT APPLICATION NUMBER: US/10/299,636  
; CURRENT FILING DATE: 2002-11-19  
; PRIOR APPLICATION NUMBER: 08/714,741  
; PRIOR FILING DATE: 1996-09-16  
; PRIOR APPLICATION NUMBER: 08/529,055  
; PRIOR FILING DATE: 1995-09-15  
; NUMBER OF SEQ ID NOS: 111  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 62  
; LENGTH: 213  
; TYPE: PRT  
; ORGANISM: Streptococcus pneumoniae  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: (2)  
; OTHER INFORMATION: Xaa at position 2 is unknown  
US-10-299-636-62

Query Match 98.1%; Score 508; DB 28; Length 213;  
Best Local Similarity 98.1%; Pred. No. 1.5e-36;  
Matches 102; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LAKKQTELEKLDNLDPBGKTQDELDKKAABAEIDKKADELPNKVADLEKEISNLEITLG 60  
Db 59 LAKKQTELEKLDNLDPBGKTQDELDKKAABAEIDKKADELPNKVADLEKEISNLEITLG 118

QY 61 GADEDDTAALPNKLTATKKALEKTOKELDALNALNELGPDGDEE 104  
Db 119 GADEDDTAALPNKLTATKKALEKTOKELDALNALNELGPDGDEE 162

RESULT 3  
US-10-674-755-20

; Sequence 20, Application US/10674755  
; GENERAL INFORMATION:

; APPLICANT: BECKER et al.  
; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE PROTEINS  
; FILE REFERENCE: 454312-2471  
; CURRENT APPLICATION NUMBER: US/10/674,755  
; CURRENT FILING DATE: 2003-09-30  
; PRIOR APPLICATION NUMBER: US/09/147,875A  
; PRIOR FILING DATE: 1999-05-24  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 20  
; LENGTH: 104  
; TYPE: PRT

; ORGANISM: Streptococcus pneumoniae  
US-10-674-755-20

Query Match 96.5%; Score 500; DB 32; Length 104;  
Best Local Similarity 97.1%; Pred. No. 2.9e-36;  
Matches 101; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LAKKQTELEKLDNLDPBGKTQDELDKKAABAEIDKKADELPNKVADLEKEISNLEITLG 60  
Db 1 LAKKQTELEKLDNLDPBGKTQDELDKKAABAEIDKKADELPNKVADLEKEISNLEITLG 60

QY 61 GADEDDTAALPNKLTATKKALEKTOKELDALNALNELGPDGDEE 104  
Db 61 GADEDDTAALPNKLTATKKALEKTOKELDALNALNELGPDGDEE 104

RESULT 4  
US-09-791-537-114569

; Sequence 114569, Application US/09791537  
; GENERAL INFORMATION:

; APPLICANT: Biomomix, Inc.  
; APPLICANT: Debe, Derek  
; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMEB  
; TITLE OF INVENTION: METHODS OF USE THEREOF  
; FILE REFERENCE: 261/210  
; CURRENT APPLICATION NUMBER: US/09/791,537  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 153055  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 114569  
; LENGTH: 502  
; TYPE: PRT  
; ORGANISM: Streptococcus pneumoniae  
US-09-791-537-114569

Query Match 96.1%; Score 498; DB 22; Length 502;  
Best Local Similarity 97.1%; Pred. No. 3.8e-35;  
Matches 101; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LAKKQTELEKLDNLDPBGKTQDELDKKAABAEIDKKADELPNKVADLEKEISNLEITLG 60  
Db 347 LAKKQTELEKLDNLDPBGKTQDELDKKAABAEIDKKADELPNKVADLEKEISNLEITLG 406

QY 61 GADEDDTAALPNKLTATKKALEKTOKELDALNALNELGPDGDEE 104  
Db 407 GADEDDTAALPNKLTATKKALEKTOKELDALNALNELGPDGDEE 450

RESULT 5  
PCT-US03-27401-251

; Sequence 251, Application PC/TUS0327401

; GENERAL INFORMATION:  
; APPLICANT: TUFTS UNIVERSITY  
; TITLE OF INVENTION: STREPTOCOCCUS PNEUMONIAE FOR DIAGNOSIS, TREATMENT AND  
; FILE REFERENCE: 700355-52941-PCT  
; CURRENT APPLICATION NUMBER: PCT/US03/27401  
; CURRENT FILING DATE: 2003-09-02  
; PRIOR APPLICATION NUMBER: US 60/407,082  
; PRIOR FILING DATE: 2002-08-30  
; NUMBER OF SEQ ID NOS: 560  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 251  
; LENGTH: 744  
; TYPE: PRT  
; ORGANISM: Streptococcus pneumoniae  
PCT-US03-27401-251

Query Match 93.4%; Score 484; DB 1; Length 744;  
Best Local Similarity 95.2%; Pred. No. 1.1e-33;  
Matches 99; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LAKKQTELEKLDNLDPPEKGTODELDKEAABAEIDKKADELPYKVADLEKEISNLEILLG 60  
Db 346 LAKKQTELEKLDNLDPPEKGTODELDKEAABAEIDKKADELPYKVADLEKEISNLEILLG 405  
Qy 61 GADPEDDTAALPNKLTATKKALEKTKQKEIDALNLEIGPDGDEE 104  
Db 406 GADSEDDTAALQNKLTATKKALEKTKQKEIDALNLEIGPDGDEE 449

## RESULT 6

US-09-769-787-184  
; Sequence 184, Application US/09769787  
; GENERAL INFORMATION:  
; APPLICANT: Microbial Technics Limited  
; APPLICANT: Gilbert, Christophe FG  
; APPLICANT: Hansbro, Philip M  
; TITLE OF INVENTION: Proteins  
; FILE REFERENCE: PWC/P21129WO  
; CURRENT APPLICATION NUMBER: US/09/769,787  
; PRIOR FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: GB 9816337.1  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: US 60/125164  
; PRIOR FILING DATE: 1999-03-19  
; NUMBER OF SEQ ID NOS: 388  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 184  
; LENGTH: 744  
; TYPE: PRT  
; ORGANISM: Streptococcus pneumoniae  
US-09-769-787-184

Query Match 93.4%; Score 484; DB 22; Length 744;  
Best Local Similarity 95.2%; Pred. No. 1.1e-33;  
Matches 99; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LAKKQTELEKLDNLDPPEKGTODELDKEAABAEIDKKADELPYKVADLEKEISNLEILLG 60  
Db 346 LAKKQTELEKLDNLDPPEKGTODELDKEAABAEIDKKADELPYKVADLEKEISNLEILLG 405  
Qy 61 GADPEDDTAALPNKLTATKKALEKTKQKEIDALNLEIGPDGDEE 104  
Db 406 GADSEDDTAALQNKLTATKKALEKTKQKEIDALNLEIGPDGDEE 449

## RESULT 7

US-10-472-928-32  
; Sequence 32, Application US/10472928  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON SPA  
; APPLICANT: THE INSTITUTE FOR GENOMIC RESEARCH  
; TITLE OF INVENTION: STREPTOCOCCUS PNEUMONIAE PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE: P026926WO  
; CURRENT APPLICATION NUMBER: US/10/472,928  
; CURRENT FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: GB-0107658.7  
; PRIOR FILING DATE: 2001-03-27  
; NUMBER OF SEQ ID NOS: 4979  
; SOFTWARE: SeqMan99, version 1.03  
; SEQ ID NO 32  
; LENGTH: 744  
; TYPE: PRT  
; ORGANISM: Streptococcus pneumoniae  
; FEATURE:  
; OTHER INFORMATION: pneumococcal surface protein A (pspa)  
; OTHER INFORMATION: Cellular location: Outside  
; OTHER INFORMATION: Feature of note: WY motif  
; OTHER INFORMATION: Similar to strain R6 sequence 15902165 (e-179)  
US-10-472-928-32

Query Match 93.4%; Score 484; DB 30; Length 744;  
Best Local Similarity 95.2%; Pred. No. 1.1e-33;  
Matches 99; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LAKKQTELEKLDNLDPPEKGTODELDKEAABAEIDKKADELPYKVADLEKEISNLEILLG 60  
Db 346 LAKKQTELEKLDNLDPPEKGTODELDKEAABAEIDKKADELPYKVADLEKEISNLEILLG 405  
Qy 61 GADPEDDTAALPNKLTATKKALEKTKQKEIDALNLEIGPDGDEE 104  
Db 406 GADSEDDTAALQNKLTATKKALEKTKQKEIDALNLEIGPDGDEE 449

## RESULT 8

US-10-873-528-184  
; Sequence 184, Application US/10873528  
; GENERAL INFORMATION:  
; APPLICANT: Microbial Technics Limited  
; APPLICANT: Gilbert, Christophe FG  
; APPLICANT: Hansbro, Philip M  
; TITLE OF INVENTION: Proteins  
; FILE REFERENCE: PWC/P21129WO  
; CURRENT APPLICATION NUMBER: US/10/873,528  
; PRIOR FILING DATE: 2004-06-23  
; PRIOR APPLICATION NUMBER: US/09/769,787  
; PRIOR FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: GB 9816337.1  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: US 60/125164  
; PRIOR FILING DATE: 1999-03-19  
; NUMBER OF SEQ ID NOS: 388  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 184  
; LENGTH: 744  
; TYPE: PRT  
; ORGANISM: Streptococcus pneumoniae  
US-10-873-528-184

Query Match 93.4%; Score 484; DB 34; Length 744;  
Best Local Similarity 95.2%; Pred. No. 1.1e-33;  
Matches 99; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LAKKQTELEKLDNLDPPEKGTODELDKEAABAEIDKKADELPYKVADLEKEISNLEILLG 60  
Db 346 LAKKQTELEKLDNLDPPEKGTODELDKEAABAEIDKKADELPYKVADLEKEISNLEILLG 405  
Qy 61 GADPEDDTAALPNKLTATKKALEKTKQKEIDALNLEIGPDGDEE 104  
Db 406 GADSEDDTAALQNKLTATKKALEKTKQKEIDALNLEIGPDGDEE 449

## RESULT 9

US-10-873-528A-184  
; Sequence 184, Application US/10873528A  
; GENERAL INFORMATION:  
; APPLICANT: Microbial Technics Limited  
; APPLICANT: Gilbert, Christophe FG  
; APPLICANT: Hansbro, Philip M  
; TITLE OF INVENTION: Proteins  
; FILE REFERENCE: PWC/P21129WO  
; CURRENT APPLICATION NUMBER: US/10/873,528A  
; CURRENT FILING DATE: 2004-06-23  
; PRIOR APPLICATION NUMBER: GB 9816337.1  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: US 60/125164  
; PRIOR FILING DATE: 1999-03-19  
; NUMBER OF SEQ ID NOS: 388  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 184  
; LENGTH: 744  
; TYPE: PRT  
; ORGANISM: Streptococcus pneumoniae  
US-10-873-528A-184

Query Match 93.4%; Score 484; DB 34; Length 744;  
Best Local Similarity 95.2%; Pred. No. 1.1e-33;

Matches 99; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 LAKQTELEKLDLNDPEGKTQDELDBKAAEAELDKKADLPNKVADLEKEISNLEILLG 60  
DB 346 LAKQTELEKLDLNDPEGKTQDELDBKAAEAELDKKADLPNKVADLEKEISNLEILLG 405

QY 61 GADPEDDTAALPNKLTATKKALEKTKQKELDAAALNELGPDGDEE 104  
DB 406 GADPEDDTAALPNKLTATKKALEKTKQKELDAAALNELGPDGDEE 449

RESULT 10  
US-08-961-083-160  
; Sequence 160, Application US/08961083  
; GENERAL INFORMATION:  
; APPLICANT: Choi et. al.  
; TITLE OF INVENTION: Streptococcus pneumoniae Antigenes and Vaccines  
; NUMBER OF SEQUENCES: 452  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: Maryland  
; COUNTRY: USA  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage  
; COMPUTER: HP Vectra 486/33  
; OPERATING SYSTEM: MSDOS version 6.2  
; SOFTWARE: ASCII Text  
; CURRENT APPLICATION NUMBER: US/08/961,083  
; FILING DATE: 30-Oct-1997  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: <Unknown>  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brookes, A. Anders  
; REGISTRATION NUMBER: 36,373  
; REFERENCE/DOCKET NUMBER: PB340P2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (301) 309-8504  
; TELEFAX: (301) 309-8512  
; INFORMATION FOR SEQ ID NO: 160:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 641 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 160:  
US-08-961-083-160

Query Match 93.2%; Score 483; DB 13; Length 641;  
Best Local Similarity 95.2%; Pred. No. 1,1e-33;  
Matches 99; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 LAKQTELEKLDLNDPEGKTQDELDBKAAEAELDKKADLPNKVADLEKEISNLEILLG 60  
DB 243 LAKQTELEKLDLNDPEGKTQDELDBKAAEAELDKKADLPNKVADLEKEISNLEILLG 302

QY 61 GADPEDDTAALPNKLTATKKALEKTKQKELDAAALNELGPDGDEE 104  
DB 303 GADPEDDTAALPNKLTATKKALEKTKQKELDAAALNELGPDGDEE 346

RESULT 11  
US-09-765-271-160  
; Sequence 160, Application US/09765271  
; GENERAL INFORMATION:  
; APPLICANT: Choi et. al.  
; TITLE OF INVENTION: Streptococcus pneumoniae Antigenes and Vaccines

NUMBER OF SEQUENCES: 452  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: Maryland  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage  
COMPUTER: HP Vectra 486/33  
OPERATING SYSTEM: MSDOS version 6.2  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/765,271  
FILING DATE: 22-Jan-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/536,784  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 08/961,083  
FILING DATE: OCT-30-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Michelle S. Marks  
REGISTRATION NUMBER: 41,971  
REFERENCE/DOCKET NUMBER: PB340P3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (301) 309-8504  
TELEFAX: (301) 309-8512  
INFORMATION FOR SEQ ID NO: 160:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 641 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 160:  
US-09-765-271-160

Query Match 93.2%; Score 483; DB 22; Length 641;  
Best Local Similarity 95.2%; Pred. No. 1,1e-33;  
Matches 99; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 LAKQTELEKLDLNDPEGKTQDELDBKAAEAELDKKADLPNKVADLEKEISNLEILLG 60  
DB 243 LAKQTELEKLDLNDPEGKTQDELDBKAAEAELDKKADLPNKVADLEKEISNLEILLG 302

QY 61 GADPEDDTAALPNKLTATKKALEKTKQKELDAAALNELGPDGDEE 104  
DB 303 GADPEDDTAALPNKLTATKKALEKTKQKELDAAALNELGPDGDEE 346

RESULT 12  
US-09-765-272-160  
; Sequence 160, Application US/09765272  
; GENERAL INFORMATION:  
; APPLICANT: Choi et. al.  
; TITLE OF INVENTION: Streptococcus pneumoniae Antigenes and Vaccines  
; NUMBER OF SEQUENCES: 452  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: Maryland  
; COUNTRY: USA  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage  
; COMPUTER: HP Vectra 486/33  
; OPERATING SYSTEM: MSDOS version 6.2  
; SOFTWARE: ASCII Text  
; CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/765,272



FILING DATE: 22-Jan-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/961,083  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Brookes, A. Anders  
REGISTRATION NUMBER: 36,373  
REFERENCE/DOCKET NUMBER: PB340P2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (301) 309-8504  
TELEFAX: (301) 309-8512  
INFORMATION FOR SEQ ID NO: 160:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 641 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 160:  
US-09-765-272-160

Query Match 93.2%; Score 483; DB 22; Length 641;  
Best Local Similarity 95.2%; Pred. No. 1.1e-33;  
Matches 99; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 LAKQTELEKLDNDLDPGKTDDELDEKAEAEALDKKADLPNKVADLEKEISNLEILLG 60  
DB 243 LAKQTELEKLDLSDLPBGKTQDELDEKAEAEALDKKADLPNKVADLEKEISNLEILLG 302

QY 61 GADPEDDTAALPNKLTATKKALEKTKOKELDAALNLELGGDDEE 104  
DB 303 GADXBDDTAALQNKLTATKKALEKTKOKELDAALNLELGGDDEE 346

RESULT 13  
US-09-765-272A-160  
Sequence 160, Application US/09765272A  
GENERAL INFORMATION:  
APPLICANT: Choi et. al.  
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and  
Vaccines  
NUMBER OF SEQUENCES: 454  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: Maryland  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage  
COMPUTER: Dell Latitude C610  
OPERATING SYSTEM: Windows 2000  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/765,272A  
FILING DATE: 22-Jan-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/961,083  
FILING DATE: OCT-30-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Lin J. Hymel  
REGISTRATION NUMBER: 45,414  
REFERENCE/DOCKET NUMBER: PB340P2C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (301) 610-5790  
TELEFAX: (301) 309-8439  
INFORMATION FOR SEQ ID NO: 160:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 641 amino acids  
TYPE: amino acid

STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 160:  
US-09-765-272A-160

Query Match 93.2%; Score 483; DB 22; Length 641;  
Best Local Similarity 95.2%; Pred. No. 1.1e-33;  
Matches 99; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 LAKQTELEKLDNDLDPGKTDDELDEKAEAEALDKKADLPNKVADLEKEISNLEILLG 60  
DB 243 LAKQTELEKLDLSDLPBGKTQDELDEKAEAEALDKKADLPNKVADLEKEISNLEILLG 302

QY 61 GADPEDDTAALPNKLTATKKALEKTKOKELDAALNLELGGDDEE 104  
DB 303 GADXBDDTAALQNKLTATKKALEKTKOKELDAALNLELGGDDEE 346

RESULT 14  
US-10-299-636-59  
Sequence 59, Application US/10299636  
GENERAL INFORMATION:  
APPLICANT: Briles, David E  
APPLICANT: McDaniel, Larry S  
APPLICANT: Swislo, Edwin  
APPLICANT: Yotner, Janet  
APPLICANT: Crain, Marilyn J  
APPLICANT: Hollingshead, Susan  
APPLICANT: Tart, Rebecca  
APPLICANT: Brooks-Walter, Alexis  
TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEINS AND USES THEREOF  
FILE REFERENCE: 57909/361  
CURRENT APPLICATION NUMBER: US/10/299,636  
CURRENT FILING DATE: 2002-11-19  
PRIOR APPLICATION NUMBER: 08/714,741  
PRIOR FILING DATE: 1996-09-16  
PRIOR APPLICATION NUMBER: 08/529,055  
PRIOR FILING DATE: 1995-09-15  
NUMBER OF SEQ ID NOS: 111  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 59  
LENGTH: 197  
TYPE: PRT  
ORGANISM: Streptococcus pneumoniae  
US-10-299-636-59

Query Match 92.7%; Score 480; DB 28; Length 197;  
Best Local Similarity 93.3%; Pred. No. 4.2e-34;  
Matches 97; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 LAKQTELEKLDNDLDPGKTDDELDEKAEAEALDKKADLPNKVADLEKEISNLEILLG 60  
DB 22 LAKQTELEKLDLSDLPBGKTQDELDEKAEAEALDKKADLPNKVADLEKEISNLEILLG 81

QY 61 GADPEDDTAALPNKLTATKKALEKTKOKELDAALNLELGGDDEE 104  
DB 82 GADXBDDTAALPNKLTATKKALEKTKOKELDAALNLELGGDDEE 125

RESULT 15  
US-10-674-755-18  
Sequence 18, Application US/10674755  
GENERAL INFORMATION:  
APPLICANT: BECKER et al.  
TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE PROTEINS  
FILE REFERENCE: 454312-2471  
CURRENT APPLICATION NUMBER: US/10/674,755  
CURRENT FILING DATE: 2003-09-30  
PRIOR APPLICATION NUMBER: US/09/147,875A  
PRIOR FILING DATE: 1999-05-24  
NUMBER OF SEQ ID NOS: 28  
SOFTWARE: PatentIn Ver. 2.1



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OM protein - protein search, using sw model

Run on: November 19, 2004, 22:20:29 ; Search time 5.07317 Seconds  
(without alignments)  
387.238 Million cell updates/sec

Title: US-10-674-755-21

Perfect score: 518  
Sequence: 1 LAKQTELEKLDNDPEK.....TKELDALNBLGPDDEE 104

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 83788 seqs, 18889656 residues

Total number of hits satisfying chosen parameters: 83788

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Pending Patents AA New:\*  
1: /cgn2\_6/ptodata/2/paa/US05\_NEW\_COMB.pep.\*  
2: /cgn2\_6/ptodata/2/paa/US07\_NEW\_COMB.pep.\*  
3: /cgn2\_6/ptodata/2/paa/US08\_NEW\_COMB.pep.\*  
4: /cgn2\_6/ptodata/2/paa/US09\_NEW\_COMB.pep.\*  
5: /cgn2\_6/ptodata/2/paa/US10\_NEW\_COMB.pep.\*  
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7: /cgn2\_6/ptodata/2/paa/US12\_NEW\_COMB.pep.\*  
8: /cgn2\_6/ptodata/2/paa/US60\_NEW\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	127	24.5	739	6	US-10-732-923-3294 Sequence 3294, Ap
2	106	20.5	882	6	US-10-732-923-3300 Sequence 3300, Ap
3	102.5	19.8	1236	6	US-10-805-684-89 Sequence 89, Appl
4	101.5	19.6	281	6	US-10-805-684-58 Sequence 58, Appl
5	99.5	19.2	865	6	US-10-732-923-7041 Sequence 7041, Ap
6	97.5	18.8	1119	6	US-10-732-923-3321 Sequence 3321, Ap
7	95.5	18.4	880	6	US-10-732-923-3314 Sequence 3314, Ap
8	95.5	18.4	1146	6	US-10-732-923-8646 Sequence 8646, Ap
9	95.5	18.4	1178	6	US-10-732-923-8641 Sequence 8641, Ap
10	93.5	18.1	339	6	US-10-805-684-59 Sequence 59, Appl
11	93.5	18.1	864	6	US-10-732-923-3312 Sequence 3312, Ap
12	93	18.0	1003	6	US-10-732-923-3319 Sequence 3319, Ap
13	93	18.0	1047	6	US-10-732-923-3320 Sequence 3320, Ap
14	92.5	17.9	1960	6	US-10-805-684-90 Sequence 90, Appl
15	92	17.8	864	6	US-10-732-923-6763 Sequence 6763, Ap
16	91.5	17.7	944	6	US-10-732-923-3333 Sequence 3333, Ap
17	91.5	17.6	858	6	US-10-732-923-6800 Sequence 6800, Ap
18	90	17.4	1939	6	US-10-732-923-3340 Sequence 3340, Ap
19	89.5	17.3	692	6	US-10-732-923-3350 Sequence 3350, Ap
20	89.5	17.3	891	6	US-10-732-923-3347 Sequence 3347, Ap
21	89.5	17.3	1043	6	US-10-732-923-535 Sequence 535, Appl
22	89	17.2	811	6	US-10-732-923-6867 Sequence 6867, Ap
23	89	17.2	899	6	US-10-732-923-6873 Sequence 6873, Ap
24	89	17.2	899	6	US-10-732-923-6874 Sequence 6874, Ap
25	89	17.2	1903	1	PCT-US04-02460-3 Sequence 3, Appl

26	88.5	17.1	284	6	US-10-979-159-273 Sequence 273, Appl
27	88.5	17.1	431	6	US-10-732-923-3348 Sequence 3348, Ap
28	88	17.0	1363	6	US-10-732-923-3336 Sequence 3336, Ap
29	88	17.0	1935	6	US-10-805-684-44 Sequence 44, Appl
30	88	17.0	1939	6	US-10-805-684-93 Sequence 93, Appl
31	88	17.0	1939	6	US-10-805-684-152 Sequence 152, Appl
32	87	16.8	1127	6	US-10-732-923-3322 Sequence 3322, Ap
33	86	16.6	296	6	US-10-967-702-149 Sequence 149, Appl
34	85.5	16.5	219	6	US-10-805-684-23 Sequence 23, Appl
35	85.5	16.5	1875	6	US-10-732-923-3334 Sequence 3334, Ap
36	85.5	16.5	1875	6	US-10-732-923-3335 Sequence 3335, Ap
37	85	16.4	1085	6	US-10-732-923-3318 Sequence 3318, Ap
38	85	16.4	1805	6	US-10-732-923-3303 Sequence 3303, Ap
39	84.5	16.3	238	6	US-10-805-684-62 Sequence 62, Appl
40	84.5	16.3	691	6	US-10-955-952-16 Sequence 16, Appl
41	84.5	16.3	691	6	US-10-157-779-16 Sequence 16, Appl
42	84.5	16.3	691	6	US-10-964-241-16 Sequence 16, Appl
43	84	16.2	713	6	US-10-959-539-52 Sequence 52, Appl
44	84	16.2	811	6	US-10-732-923-6868 Sequence 6868, Ap
45	84	16.2	886	6	US-10-732-923-3310 Sequence 3310, Ap

#### ALIGNMENTS

```
RESULT 1
US-10-732-923-3294
; Sequence 3294, Application US/10732923
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; PRIOR APPLICATION NUMBER: 2003-12-10
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 3294
; LENGTH: 739
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-732-923-3294

Query Match      24.5%; Score 127; DB 6; Length 739;
Best Local Similarity 34.8%; Pred. No. 0.0004;
Matches 40; Conservative 15; Mismatches 40; Indels 20; Gaps 3;

QY      1 LAKQTELEKLDNDPEKTDDELD-----KEAAEELDKKAD-----ELPNKV 45
DB      519 LEAKTAELREYQRLKEKEIDSDYLGKGRAPLOSKLDTKKAKLSTLBEISDKT 578
      46 ADLEKEISNLEILLGADPEDDTAA-----LPNKLATKKALEKTOKEIDALNE 95
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      579 DELDAEIKAKYQLQDABGNNVVEAYFKEGLEKTTAAKKAKAEKAEADLKKAVDE 633

RESULT 2
US-10-732-923-3300
; Sequence 3300, Application US/10732923
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; PRIOR APPLICATION NUMBER: 2003-12-10
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 3300
; LENGTH: 882
; TYPE: PRT
; ORGANISM: Pyrococcus furiosus DSM 3638
US-10-732-923-3300
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Query Match 20.5%; Score 106; DB 6; Length 882;  
Best Local Similarity 29.1%; Pred. No. 0.036;  
Matches 33; Conservative 25; Mismatches 35; Indels 18; Gaps 4;

QY 1 LAKQTELEKLDNDPEGKTODELDKEAAEAELDKKADELPNKVADELKEISNLEILLGA 51  
DB 318 IREKLTVEELINIQ---KRIBELNKESEKLEENKEKELINKLAILKEDHQLYEIK 374  
QY 52 -----ISNLSILGADPEDDTALPNKLTATKKALEKTQKELDAALNEL 96  
DB 375 AKKENLQKLEKLGDKSPF-DIKKDLLELETKTTEEBERNETIORIGEL 423

RESULT 3  
US-10-805-684-89  
; Sequence 89, Application US/10805684  
; GENERAL INFORMATION:  
; APPLICANT: SAKAMOTO, TAKESHI  
; APPLICANT: TAKEDA, SHIZU  
; TITLE OF INVENTION: PHOS-INTERACTING PROTEINS AND USE THEREOF  
; FILE REFERENCE: 58748(70342)  
; CURRENT APPLICATION NUMBER: US/10/805,684  
; CURRENT FILING DATE: 2004-03-19  
; PRIOR APPLICATION NUMBER: 60/455,766  
; PRIOR FILING DATE: 2003-03-19  
; PRIOR APPLICATION NUMBER: 60/459,936  
; PRIOR FILING DATE: 2003-04-02  
; PRIOR APPLICATION NUMBER: 60/460,103  
; PRIOR FILING DATE: 2003-04-02  
; NUMBER OF SEQ ID NOS: 161  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 89  
; LENGTH: 1236  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-805-684-89

Query Match 19.8%; Score 102.5; DB 6; Length 1236;  
Best Local Similarity 27.0%; Pred. No. 0.11;  
Matches 30; Conservative 25; Mismatches 37; Indels 19; Gaps 3;

QY 3 KKQTELEKLDNDPEGKTODELDKEAAEAELDKKADELPNKVADELKEISNLEILLGA 62  
DB 291 KQEWIMSDLEERLKKERKTRQLEK--AKRKLDSGTTDLDQIAELQAVDELKVQLTKK 348  
QY 63 DPE-----DPTALPNKLTATKKALEKTQKELDAALNELGPDDEER 104  
DB 349 EEEIQLALRGDDDTLHKNNAL-----KVARELQAIQIAELQEDFESEK 391

RESULT 4  
US-10-805-684-58  
; Sequence 58, Application US/10805684  
; GENERAL INFORMATION:  
; APPLICANT: SAKAMOTO, TAKESHI  
; APPLICANT: TAKEDA, SHIZU  
; TITLE OF INVENTION: PHOS-INTERACTING PROTEINS AND USE THEREOF  
; FILE REFERENCE: 58748(70342)  
; CURRENT APPLICATION NUMBER: US/10/805,684  
; CURRENT FILING DATE: 2004-03-19  
; PRIOR APPLICATION NUMBER: 60/455,766  
; PRIOR FILING DATE: 2003-03-19  
; PRIOR APPLICATION NUMBER: 60/459,936  
; PRIOR FILING DATE: 2003-04-02  
; PRIOR APPLICATION NUMBER: 60/460,103  
; PRIOR FILING DATE: 2003-04-02  
; NUMBER OF SEQ ID NOS: 161  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 58  
; LENGTH: 281  
; TYPE: PRT  
; ORGANISM: Mus musculus

US-10-805-684-58

Query Match 19.6%; Score 101.5; DB 6; Length 281;  
Best Local Similarity 27.0%; Pred. No. 0.024;  
Matches 30; Conservative 25; Mismatches 37; Indels 19; Gaps 3;

QY 3 KKQTELEKLDNDPEGKTODELDKEAAEAELDKKADELPNKVADELKEISNLEILLGA 62  
DB 165 KQEWIMSDLEERLKKERKTRQLEK--AKRKLDSGTTDLDQIAELQAVDELKVQLTKK 222  
QY 63 DPE-----DPTALPNKLTATKKALEKTQKELDAALNELGPDDEER 104  
DB 223 EEEIQLALRGDDDTLHKNNAL-----KVARELQAIQIAELQEDFESEK 265

RESULT 5  
US-10-732-923-7041  
; Sequence 7041, Application US/10732923  
; GENERAL INFORMATION:  
; APPLICANT: Edgerton, Michael D  
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES  
; FILE REFERENCE: 38-15(52796)C  
; CURRENT APPLICATION NUMBER: US/10/732,923  
; CURRENT FILING DATE: 2003-12-10  
; PRIOR APPLICATION NUMBER: 10/310,154  
; PRIOR FILING DATE: 2002-12-04  
; NUMBER OF SEQ ID NOS: 24149  
; SEQ ID NO 7041  
; LENGTH: 865  
; TYPE: PRT  
; ORGANISM: Clostridium tetani E88  
US-10-732-923-7041

Query Match 19.2%; Score 99.5; DB 6; Length 865;  
Best Local Similarity 30.6%; Pred. No. 0.13;  
Matches 33; Conservative 20; Mismatches 28; Indels 27; Gaps 5;

QY 5 QTELEKLDNDPEGKT--ODELDKEAAEAELDKKADELPNKVADELKEISNLEILLGA 62  
DB 406 RTEIDSLPTELDLSKRIKIFQMEIEKELAKEDSRSGE---RLDELEKESLNK----- 456  
QY 63 DPEDDTAA-----LPNKLTATKKALEKTQKELDAALNEL 96  
DB 457 EKQEWIMAKYEKEKEQIINRNKIKQKLDVYKQLEKAREYD--LNKV 502

RESULT 6  
US-10-732-923-3321  
; Sequence 3321, Application US/10732923  
; GENERAL INFORMATION:  
; APPLICANT: Edgerton, Michael D  
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES  
; FILE REFERENCE: 38-15(52796)C  
; CURRENT APPLICATION NUMBER: US/10/732,923  
; CURRENT FILING DATE: 2003-12-10  
; PRIOR APPLICATION NUMBER: 10/310,154  
; PRIOR FILING DATE: 2002-12-04  
; NUMBER OF SEQ ID NOS: 24149  
; SEQ ID NO 3321  
; LENGTH: 1119  
; TYPE: PRT  
; ORGANISM: Daucus carota  
US-10-732-923-3321

Query Match 18.8%; Score 97.5; DB 6; Length 1119;  
Best Local Similarity 27.2%; Pred. No. 0.27;  
Matches 34; Conservative 28; Mismatches 32; Indels 31; Gaps 6;

QY 2 AKQTELEKLDNDPEGKTODELDKEAAEAELDKK---ADELPNKVADELK---EISN 54  
DB 289 AREQSEIQKLID---EHKAILLEVYKQSFEMENDKRNDFQNNQNAVEVEKKEVEVKH 344  
QY 55 LEILLGADPEDDTALPNK-----LATKKALEKTQKELDAALNELGPD----- 99

Db 345 LEAKLAKRE-----HLDQGEKLEKEQYLASKLDLNERKSMKLEBKIDENQUL 399  
 QY 100 GDEEE 104  
 Db 400 SDKOE 404

## RESULT 7

US-10-732-923-3314  
 ; Sequence 3314, Application US/10732923  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Edgerton, Michael D  
 ; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES  
 ; FILE REFERENCE: 38-15(52796)C  
 ; CURRENT APPLICATION NUMBER: US/10/732,923  
 ; CURRENT FILING DATE: 2003-12-10  
 ; PRIOR APPLICATION NUMBER: 10/310,154  
 ; PRIOR FILING DATE: 2002-12-04  
 ; NUMBER OF SEQ ID NOS: 24149  
 ; SEQ ID NO 3314  
 ; LENGTH: 880  
 ; TYPE: PRT  
 ; ORGANISM: Pyrococcus abyssi  
 US-10-732-923-3314

Query Match 18.4%; Score 95.5; DB 6; Length 880;  
 Best Local Similarity 28.8%; Pred. No. 0.31;  
 Matches 30; Conservative 24; Mismatches 33; Indels 17; Gaps 4;

QY 1 LAKKOTLEKLDNDPEKTODELKKAEE--AEIDKKADELPNKVADL-----KXI 52  
 Db 320 LKMBSEL-KALBEVAKESGKKERAEIRKLSIEIKLBEKPYVELEDAKQVQKI 378  
 QY 53 SNLEILLGGADEPDDTALPNKLTATKKALEKTOKELDALNEL 96  
 Db 379 ERLKARLKGLS-----PGEVTEKLESEKERTIEBAIKXI 414

## RESULT 8

US-10-732-923-8646  
 ; Sequence 8646, Application US/10732923  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Edgerton, Michael D  
 ; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES  
 ; FILE REFERENCE: 38-15(52796)C  
 ; CURRENT APPLICATION NUMBER: US/10/732,923  
 ; CURRENT FILING DATE: 2003-12-10  
 ; PRIOR APPLICATION NUMBER: 10/310,154  
 ; PRIOR FILING DATE: 2002-12-04  
 ; NUMBER OF SEQ ID NOS: 24149  
 ; SEQ ID NO 8646  
 ; LENGTH: 1146  
 ; TYPE: PRT  
 ; ORGANISM: Neurospora crassa  
 US-10-732-923-8646

Query Match 18.4%; Score 95.5; DB 6; Length 1146;  
 Best Local Similarity 30.5%; Pred. No. 0.42;  
 Matches 29; Conservative 19; Mismatches 36; Indels 11; Gaps 3;

QY 8 LEKLDNDPEKTODELKKAEEALDKKADLPNKVADLEKEISNLEIL-LGGADPED 66  
 Db 957 LEQENAKMEAEKETEDD-DDENDSTWVTDDDDDETVDLERAVANBEILVLGSEKPA 1015  
 QY 67 DTAALPNKLTATKKALEKTOKELDALNELGPGD 101  
 Db 1016 GVEVTRGEIAEKRAV-----AGAAERGBEGD 1041

RESULT 9  
 US-10-732-923-8641  
 ; Sequence 8641, Application US/10732923

; GENERAL INFORMATION:  
 ; APPLICANT: Edgerton, Michael D  
 ; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES  
 ; FILE REFERENCE: 38-15(52796)C  
 ; CURRENT APPLICATION NUMBER: US/10/732,923  
 ; CURRENT FILING DATE: 2003-12-10  
 ; PRIOR APPLICATION NUMBER: 10/310,154  
 ; PRIOR FILING DATE: 2002-12-04  
 ; NUMBER OF SEQ ID NOS: 24149  
 ; SEQ ID NO 8641  
 ; LENGTH: 1178  
 ; TYPE: PRT  
 ; ORGANISM: Neurospora crassa  
 US-10-732-923-8641

Query Match 18.4%; Score 95.5; DB 6; Length 1178;  
 Best Local Similarity 30.5%; Pred. No. 0.43;  
 Matches 29; Conservative 19; Mismatches 36; Indels 11; Gaps 3;

QY 8 LEKLDNDPEKTODELKKAEEALDKKADLPNKVADLEKEISNLEIL-LGGADPED 66  
 Db 989 LEQENAKMEAEKETEDD-DDENDSTWVTDDDDDETVDLERAVANBEILVLGSEKPA 1047  
 QY 67 DTAALPNKLTATKKALEKTOKELDALNELGPGD 101  
 Db 1048 GVEVTRGEIAEKRAV-----AGAAERGBEGD 1073

## RESULT 10

US-10-805-684-59  
 ; Sequence 59, Application US/10805684  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SAKAMOTO, TAKESHI  
 ; APPLICANT: TAKEDA, SHIZU  
 ; TITLE OF INVENTION: FOS-INTERACTING PROTEINS AND USE THEREOF  
 ; FILE REFERENCE: 58748(70342)  
 ; CURRENT APPLICATION NUMBER: US/10/805,684  
 ; CURRENT FILING DATE: 2004-03-19  
 ; PRIOR APPLICATION NUMBER: 60/455,766  
 ; PRIOR FILING DATE: 2003-03-19  
 ; PRIOR APPLICATION NUMBER: 60/459,936  
 ; PRIOR FILING DATE: 2003-04-02  
 ; PRIOR APPLICATION NUMBER: 60/460,103  
 ; PRIOR FILING DATE: 2003-04-02  
 ; NUMBER OF SEQ ID NOS: 161  
 ; SOFTWARE: Patencin Ver. 3.2  
 ; SEQ ID NO 59  
 ; LENGTH: 339  
 ; TYPE: PRT  
 ; ORGANISM: Mus musculus  
 US-10-805-684-59

Query Match 18.1%; Score 93.5; DB 6; Length 339;  
 Best Local Similarity 27.5%; Pred. No. 0.16;  
 Matches 30; Conservative 29; Mismatches 41; Indels 9; Gaps 4;

QY 1 LAKKOTLEKLDNDP-----EGKTODELKKAEEALDKKADLPNKVADLEKEISNLE 56  
 Db 166 LAKLNKKEHAMITDLEERLRREKORQELKTRKLEGD--STDSDQIAEQAQIAELK 223  
 QY 57 ILLGADPEDDT--AALPNKLTATKKALEKTOKELDALNELGPGDDE 103  
 Db 224 MQLAKKEBSQALALARVEEAAQKMAALKI-RELETOISLEQEDLESE 271

## RESULT 11

US-10-732-923-3312  
 ; Sequence 3312, Application US/10732923  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Edgerton, Michael D  
 ; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES  
 ; FILE REFERENCE: 38-15(52796)C  
 ; CURRENT APPLICATION NUMBER: US/10/732,923

```

; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 3312
; LENGTH: 864
; TYPE: PRT
; ORGANISM: Sulfolobus solfataricus
US-10-732-923-3312

```

```

Query Match      18.1%; Score 93.5; DB 6; Length 864;
Best Local Similarity 31.9%; Pred. No. 0.46;
Matches 36; Conservative 16; Mismatches 32; Indels 29; Gaps 5;

```

```

QY 1 LAKQTELEKLDNDPEPGKQDELDK-----AAEALDK---KA 38
DB 494 LKJNEIEIENHSHIESIKNDSEIKKINEVEKELKYEEFMFLSKYTKEDLKKVKL 553
QY 39 DELPNKVADEKEISNLEILGADPEDDTAALPNK--LATKKALEKTOKE 88
DB 554 DEMKKKEEIEKEMRGLSELEKGLDRK---ALSKLIDLENKRVKLDMMKK 602

```

```

RESULT 12
US-10-732-923-3319
; Sequence 3319, Application US/10732923
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 3319
; LENGTH: 1003
; TYPE: PRT
; ORGANISM: Kaposi's sarcoma-associated herpesvirus
US-10-732-923-3319

```

```

Query Match      18.0%; Score 93; DB 6; Length 1003;
Best Local Similarity 25.5%; Pred. No. 0.6;
Matches 27; Conservative 27; Mismatches 44; Indels 8; Gaps 2;

```

```

QY 1 LAKQTELEKLDNDPEPGKQDELDK--EAAEALDKKADLPNKVADLEKISNLEIL 58
DB 600 LEEQOELEEQOELEEQOELEEQOELEEQOELEEQOELEEQOELEEQOELE-- 657
QY 59 LGADPEDDTAALPNKLATKKALEKTOKEIDAALNLELGPDDDEE 104
DB 658 -----EQOELEEQOELEEQOELEEQOELEEQOELEEQOELEEQOELE 699

```

```

RESULT 13
US-10-732-923-3320
; Sequence 3320, Application US/10732923
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 3320
; LENGTH: 1047
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1) ... (1047)

```

```

; OTHER INFORMATION: unsure at all Xaa locations
US-10-732-923-3320

```

```

Query Match      18.0%; Score 93; DB 6; Length 1047;
Best Local Similarity 27.5%; Pred. No. 0.63;
Matches 38; Conservative 26; Mismatches 34; Indels 40; Gaps 7;

```

```

QY 2 AKQTELEKLDNDPEPGKQDELDKAAEALDK-----ADELPNKVADLEK---EISN 54
DB 209 AREKVEHQKLD-----EQNTILDVKKQFEVELDEKRSKSPEDGLKNLVEVEKKEALITH 264
QY 55 LE-----ILG-----GADPEDDTAALPNK-----LATKKALEKTOKE 88
DB 265 MEKVAKRQALGKAKLEKEIEYEQVKALREKELIKSEBKSIVTEKGIKIESEREB 324
QY 89 L---DAALNLELGPDDDEE 103
DB 325 LETHRAVEKIRANNEE 342

```

```

RESULT 14
US-10-805-684-90
; Sequence 90, Application US/10805684
; GENERAL INFORMATION:
; APPLICANT: SAKAMOTO, TAKESHI
; APPLICANT: TAKEDA, SHIZU
; TITLE OF INVENTION: PHOS-INTERACTING PROTEINS AND USE THEREOF
; FILE REFERENCE: 58748(70342)
; CURRENT APPLICATION NUMBER: US/10/805,684
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: 60/455,766
; PRIOR FILING DATE: 2003-03-19
; PRIOR APPLICATION NUMBER: 60/459,936
; PRIOR FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 60/460,103
; PRIOR FILING DATE: 2003-04-02
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 90
; LENGTH: 1960
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-805-684-90

```

```

Query Match      17.9%; Score 92.5; DB 6; Length 1960;
Best Local Similarity 27.0%; Pred. No. 1.4;
Matches 27; Conservative 25; Mismatches 37; Indels 11; Gaps 3;

```

```

QY 5 QTELEKLDNDPEPGKQDELDKAAEALDKKADLPNKVADLEKIS-----NLEI 57
DB 1503 RTEMEDLMSKVDVGSVHELEK--SKRALQQVEEMKQLELEDELQATEDAKLRLEV 1560
QY 58 ILGG--ADPEDDTAALPNKLATKKALEKTOKEIDAALNE 95
DB 1561 NLQAMKAQFERDLOGRDEQSEKKQLVQVREWEALIED 1600

```

```

RESULT 15
US-10-732-923-6763
; Sequence 6763, Application US/10732923
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 6763
; LENGTH: 864
; TYPE: PRT
; ORGANISM: Fusobacterium nucleatum subsp. nucleatum ATCC 25586

```

US-10-732-923-6763

Query Match	17.8%;	Score 92;	DB 6;	Length 864;
Best Local Similarity	28.1%;	Pred NO	0.63;	

Matches 34; Conservative 23; Mismatches 36; Indels 28; Gaps 5;

QY 1 LAKKOTELEKLLDNLDPBEGTQDE-----LDKEAEAEELDKA-----DELPNKV 45

QY 1 LAKKQTELEKLDNLDPEGKTQDE-----LDKEAAEAELDKKA-----DELPNKV 45

Db 420 LTRKALQLEIKALEKE--TDDASKERLVIKELAELENEKKVLTSMWELEKEDISKI 477

46 ADLEKEISNLEILLGGADPEDDTAALP---NKLATKAELEKTQKELDPAALNELGPPDG 101

Db 478 KNIKREIENVKLEMEKAREYDTLTKSELTKYGLATLEKELQEQONKVD-----KQKG 530

QY 102 E 102

Db 531 E 531

Search completed: November 19, 2004, 23:18:04  
Job time : 6.07317 secs

Job time : 6.07317 secs

**This Page Blank (uspto)**



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using SW model

Run on: November 19, 2004, 22:05:43 ; Search time 13.9512 Seconds  
(without alignment)

717.252 Million cell updates/sec

Title: US-10-674-755-21

Perfect score: 518  
Sequence: 1 LAKKQTELEKLDNDPBEK.....TKKELDAALNELGPDDEE 104

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:\*

1: p1r1:\*

2: p1r2:\*

3: p1r3:\*

4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	484	93.4	744	2 P95013	pneumococcal surfa
2	128	24.7	619	2 A97887	surface protein ps
3	128	24.7	619	2 A41971	myosin heavy chain
4	109.5	21.1	924	2 S06117	myosin heavy chain
5	109.5	21.1	2007	1 B43402	hypothetical prote
6	104	20.1	281	2 F75216	hypothetical prote
7	103.5	20.0	388	2 A46173	Mtp4 protein - Str
8	103.5	20.0	1938	1 A40997	myosin heavy chain
9	103.5	20.0	1976	2 A59252	myosin heavy chain
10	103	19.9	397	2 H86754	prophage p12 prote
11	101	19.5	2139	2 T18296	myosin heavy chain
12	100.5	19.4	527	2 S33068	myosin heavy chain
13	100.5	19.4	1509	1 A27224	myosin heavy chain
14	100.5	19.4	1940	2 A59287	myosin heavy chain
15	100	19.3	259	2 D60110	repetitive protein
16	100	19.3	385	2 T20410	hypothetical prote
17	100	19.3	1837	2 T41023	probable nuclear p
18	99.5	19.2	1992	2 A47297	myosin heavy chain
19	99	19.1	199	2 A61513	myosin, sarcomeric
20	99	19.1	388	2 S52536	fcra 15 protein -
21	98.5	19.0	1964	2 A59282	nonmuscle myosin I
22	98	18.9	415	2 S35760	myosin heavy chain
23	97.5	18.8	1119	2 T14321	nuclear matrix con
24	97.5	18.8	1172	1 A41604	myosin heavy chain
25	97.5	18.8	2346	2 T13829	myosin heavy chain
26	97	18.7	518	2 G84488	En/Spm-like transp
27	97	18.7	587	2 JCL119	Fc gamma (1g) rec
28	97	18.7	936	2 S39083	myosin heavy chain
29	97	18.7	1957	2 A59294	skeletal myosin -

30	96.5	18.6	405	2 A33939	Fc gamma (1g) rec
31	96.5	18.6	629	2 T44607	hypothetical prote
32	96	18.5	1169	2 A64505	p15 homolog - Met
33	96	18.5	1175	2 C35815	myosin heavy chain
34	96	18.5	1175	2 D35815	myosin heavy chain
35	96	18.5	1201	2 A35815	myosin heavy chain
36	96	18.5	1201	2 B35815	myosin heavy chain
37	96	18.5	1313	2 A48467	myosin heavy chain
38	96	18.5	2385	2 A32491	myosin heavy chain
39	96	18.5	2411	2 B32491	myosin heavy chain
40	95.5	18.4	880	2 F75103	conserved hypotet
41	95.5	18.4	1163	2 F84669	probable chromosom
42	95.5	18.4	1937	2 I38055	myosin heavy chain
43	95.5	18.4	1938	2 JC5421	smooth muscle myos
44	95.5	18.4	1972	2 UC5420	smooth muscle myos
45	95	18.3	516	2 B84709	hypothetical prote

## ALIGNMENTS

RESULT 1  
P95013  
pneumococcal surface protein A [imported] - Streptococcus pneumoniae (strain TIGR4)  
C:Species: Streptococcus pneumoniae  
C:Date: 03-Aug-2001 #sequence\_revision 03-Aug-2001 #ext\_change 09-Jul-2004  
C:Accession: P95013  
R:/tettelin, H.; Neilson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Hel-  
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,  
nson, T.; Hickey, E.K.; Holt, I.E.  
Science 293, 498-506, 2001  
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison  
A:/Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.  
A:/Reference number: A95000; MUID:21537209; PMID:11463916  
A:/Accession: P95013  
A:/Status: preliminary  
A:/Molecule type: DNA  
A:/Residues: 1-744 <KUR>  
A:/Cross-references: UNIPROT:Q97739; GB:AEO05672; PIDN:AAK74303.1; PID:G14971584; GSPDB:  
A:/Experimental source: strain TIGR4  
C:/Genetics:  
A:/Gene: SP0117

Query Match 93.4%; Score 484; DB 2; Length 744;  
Best Local Similarity 95.2%; Pred. No. 2.9e-26;  
Matches 99; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 LAKKQTELEKLDNDPBEKTDDEKAEAEALDKKADLPNKVADLEKEISNLEITLG 60  
DB 346 LAKKQTELEKLDNDPBEKTDDEKAEAEALDKKADLPNKVADLEKEISNLEITLG 405

QY 61 GADPEDDTAALPNKATKKALEKTKQKELDAALNELGPDDEE 104  
DB 406 GADSEDDTAALQNKATKKALEKTKQKELDAALNELGPDDEE 449

RESULT 2  
A97887  
surface protein pspA precursor [imported] - Streptococcus pneumoniae (strain R6)  
C:Species: Streptococcus pneumoniae  
C:Date: 22-Oct-2001 #sequence\_revision 22-Oct-2001 #ext\_change 09-Jul-2004  
C:/Accession: A97887  
R:/Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; Dehoff, B.S.; E-  
e, R.; Leblanc, D.J.; Lee, L.N.; Letkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; f  
Y, P.; Sun, P.M.; Winkler, M.E.  
J. Bacteriol. 183, 5709-5717, 2001  
A:/Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaekunas, S.R.,  
A:/Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.  
A:/Reference number: A97887; MUID:21429245; PMID:11544234  
A:/Accession: A97887  
A:/Status: preliminary  
A:/Molecule type: DNA  
A:/Residues: 1-619 <KUR>

A/Cross-references: UNIPROT:Q54972; UNIPROT:Q8DR10; GB:AE007317; PIDN:AAK98925.1; PID:G1  
C:Genetics:  
A:Gene: psppa

Query Match 24.7%; Score 128; DB 2; Length 619;  
Best Local Similarity 34.8%; Pred. No. 0.09;  
Matches 39; Conservative 15; Mismatches 38; Indels 20; Gaps 3;

Qy 4 KQTELEKLDNLDEGKTODELD-----KEAAEAELDKKAD-----ELPNKAVDL 48  
Db 208 KIAELNQHVRHLEQLEKIDSESDYAKGFRAPLQSKLDAAKAKLSKEELSDKIDEL 267

Qy 49 EKEISNLEILLGADPEDDT-----AALPNKLTATKKALEKTOKELDPAALNE 95  
Db 268 DAEIAXKEDQKAAEENNNDYDFKEGLEKRTIAAKKALEKTEADLKAVANE 319

RESULT 3  
A41971  
surface protein psppa precursor - Streptococcus pneumoniae  
N/Alternate names: pneumococcal surface protein A  
C/Species: Streptococcus pneumoniae  
C/Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C/Accession: A41971; A60282; A3134  
R/Yother, J.; Briles, D.B.  
J. Bacteriol. 174, 601-609, 1992  
A/Title: Structural properties and evolutionary relationships of PsppA, a surface protein  
A/Reference numbers: A41971; MUID:92105030; PMID:11729249  
A/Accession: A41971  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-619 <YOT>  
A/Cross-references: UNIPROT:Q54972; UNIPROT:Q8DR10; GB:M74122; NID:G153840; PIDN:AAA2701  
A/Note: sequence extracted from NCBI backbone (NCBI:75635, NCBI:75636)  
R/talkington, D.F.; Crimmins, D.L.; Voellinger, D.C.; Yother, J.; Briles, D.B.  
Infect. Immun. 59, 1285-1289, 1991  
A/Title: A 43-kilodalton pneumococcal surface protein, PsppA: isolation, protective ability  
A/Reference numbers: A60282; MUID:91169598; PMID:2004810  
A/Accession: A60282  
A/Molecule type: protein  
A/Residues: 32-76 <TAL>  
A/Experimental source: strain JY2008  
C/Genetics:  
A:Gene: psppa  
F:1-31/Domain: signal sequence #status predicted <SIG>  
F:32-61/Domain: surface protein psppa #status predicted <MAT>  
F:411-430/Domain: cpl repeat homology <CP01>  
F:431-450/Domain: cpl repeat homology <CP02>  
F:451-470/Domain: cpl repeat homology <CP03>  
F:471-490/Domain: cpl repeat homology <CP04>  
F:491-510/Domain: cpl repeat homology <CP05>  
F:511-530/Domain: cpl repeat homology <CP06>  
F:531-550/Domain: cpl repeat homology <CP07>  
F:551-570/Domain: cpl repeat homology <CP08>  
F:571-591/Domain: cpl repeat homology <CP09>  
F:592-611/Domain: cpl repeat homology <CP10>

Query Match 24.7%; Score 128; DB 2; Length 619;  
Best Local Similarity 34.8%; Pred. No. 0.09;  
Matches 39; Conservative 15; Mismatches 38; Indels 20; Gaps 3;

Qy 4 KQTELEKLDNLDEGKTODELD-----KEAAEAELDKKAD-----ELPNKAVDL 48  
Db 208 KIAELNQHVRHLEQLEKIDSESDYAKGFRAPLQSKLDAAKAKLSKEELSDKIDEL 267

Qy 49 EKEISNLEILLGADPEDDT-----AALPNKLTATKKALEKTOKELDPAALNE 95  
Db 268 DAEIAXKEDQKAAEENNNDYDFKEGLEKRTIAAKKALEKTEADLKAVANE 319

RESULT 4  
S06117  
myosin heavy chain, nonmuscle (clone lambda-FMHC) - chicken (fragment)

C/Species: Gallus gallus (chicken)  
C/Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 09-Jul-2004  
C/Accession: S06117  
R/Katsuragawa, Y.; Yanagisawa, M.; Inoue, A.; Masaki, T.  
Eur. J. Biochem. 184, 611-616, 1989  
A/Title: Two distinct nonmuscle myosin-heavy-chain mRNAs are differentially expressed in  
s.  
A/Reference numbers: S06116; MUID:90032648; PMID:2806244  
A/Accession: S06117  
A/Status: not compared with conceptual translation  
A/Molecule type: mRNA  
A/Residues: 1-924 <KAT>  
A/Cross-references: UNIPROT:Q02015; GB:X17590  
A/Note: this translation is not annotated in GenBank entry GGMHCFC, release 114  
C/Superfamily: myosin heavy chain; myosin motor domain homology  
F:1-303/Domain: myosin motor domain homology (fragment) <MOT>

Query Match 21.1%; Score 109.5; DB 2; Length 924;  
Best Local Similarity 31.2%; Pred. No. 2.6;  
Matches 34; Conservative 27; Mismatches 41; Indels 7; Gaps 3;

Qy 1 LAKQTELEKLDNLDEGKTODELDKEAAEAELDKKADLPKRVADLEKISNLE 56  
Db 557 LAKLKNQEMWITDLERLKEEKTRQELK--AKRKLDSSTTDLQDQIALQELQLELK 614

Qy 57 ILLGADPEDDTA-ALPNKLTATKKALEKTOKELDPAALNEIGPDGDEE 104  
Db 615 IQLAKKEELQALARDDEAVQNNMLKYIRLQALQALQELQLESEK 663

RESULT 5  
B43402  
myosin heavy chain-B, neuronal - chicken  
N/Contains: myosin ATPase (BC 3.6.4.1)  
C/Species: Gallus gallus (chicken)  
C/Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004  
C/Accession: B43402; A43402  
R/Takahashi, M.; Kawamoto, S.; Adelstein, R.S.  
J. Biol. Chem. 267, 17864-17871, 1992  
A/Title: Evidence for inserted sequences in the head region of nonmuscle myosin specific  
yosin.  
A/Reference numbers: A43402; MUID:92388144; PMID:1355479  
A/Accession: B43402  
A/Molecule type: mRNA  
A/Residues: 1-2007 <TAK>  
A/Cross-references: UNIPROT:Q02015; GB:M93676; NID:G212448; PIDN:AAA48988.1; PID:G212452  
A/Note: the sequence of residues 212-221 and 632-652 and the corresponding nucleotide seq  
A/Accession: A43402  
A/Molecule type: mRNA  
A/Residues: 1-211,222-631,653-2007 <TA2>  
A/Cross-references: GB:M93676; NID:G212448; PIDN:AAA48985.1; PID:G212449  
A/Note: sequence extracted from NCBI backbone (NCBI:112864)  
C/Comment: Alternatively spliced segments 1 and 2 are found exclusively in nonmuscle myot  
C/Keywords: actin binding; myosin heavy chain; myosin motor domain homology  
F:1-2007/Product: myosin heavy chain-B, neuronal #status predicted <MYN>  
F:1-211,222-631,653-2007/Product: myosin heavy chain-B, nonmuscle #status predicted <MYS>  
F:88-802/Domain: myosin motor domain homology <MOT>  
F:178-185/Region: nucleotide-binding motif A (P-loop)  
F:212-221/Region: alternatively spliced segment 1 #status experimental  
F:559-593/Region: actin binding #status predicted  
F:632-652/Region: alternatively spliced segment 2 #status experimental  
F:659-714/Region: actin binding #status predicted  
F:875-2007/Domain: coiled coil #status predicted <COI>  
F:875-1315/Region: S2  
F:1316-2007/Region: light meromyosin  
F:129/Modified site: N6, N6, N6-trimethyllysine (Lys) #status predicted  
F:184/Binding site: ATP (Lys) #status predicted  
F:732,742/Active site: Cys #status predicted  
F:1954/Binding site: phosphate (Thr) (covalent) #status predicted  
F:1987/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 21.1%; Score 109.5; DB 1; Length 2007;



R:Meir, L.  
submitted to the EMBL Data Library, August 1995  
A:Reference number: H00753  
A:Accession: G02055  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-81 <MEI>  
A:Cross-references: EMBL:U34304; NID:G1143217; PIDN:AAA84880.1; PID:G1143218  
C:Genetics:  
A:Gene: GDB:MYH10  
A:Cross-references: GDB:127350; GDB:G00-127-350; OMIM:160776  
A:Map position: 17p13-17p13  
C:Superfamily: myosin heavy chain; myosin motor domain homology  
C:Keywords: actin binding; ATP; coiled coil; hydrolyase; methylated amino acid; nucleotide  
F:88-771/Domain: myosin motor domain homology <MMO>  
F:178-185/Region: nucleotide-binding motif A (P-loop)  
F:559-572/Region: actin binding #status predicted  
F:633-647/Region: actin binding #status predicted  
F:129/Modified site: N6, N6, N6-trimethyllysine (Lys) #status predicted  
F:184/Binding site: ATP (Lys) #status predicted  
F:701,711/Active site: Cys #status predicted

Query Match 20.0%; Score 103.5; DB 2; Length 1976;  
Best Local Similarity 27.9%; Pred. No. 15;  
Matches 31; Conservative 24; Mismatches 37; Indels 19; Gaps 3;

QY 3 KKQTELEKLDNLDPEGKTQDELKKAELDKKADLPNKVADLEKEISNLEILGGA 62  
DB 1031 KQEWISDLEERLKEETKROELK--AKRKLDSITTDLQOQIALQIDELKQLAKK 1088

QY 63 DPE-----DDTALPNKLTATKAELEKTELDAALNGLPGDDEE 104  
DB 1089 EEEGLALARGDDFTLHKNNNL-----KVRLELQALIELQEDFESK 1131

RESULT 10  
H86754  
prophage p12 protein 33, capsid protein [imported] - Lactococcus lactis subsp. lactis (B  
C:Species: Lactococcus lactis subsp. lactis  
C:Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 09-Jul-2004  
C:Accession: H86754  
R:Boletín, A.; Wincker, P.; Manger, S.; Jallón, O.; Malarme, K.; Weissenbach, J.; Ehrlich  
Genome Res. 11, 731-753, 2001  
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s8  
A:Reference number: A86625; MUID:21235186; PMID:11337471  
A:Accession: H86754  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-397 <STO>  
A:Cross-references: UNIPROT:Q9CGQ6; GB:AE005176; PID:G1272392; PIDN:AAK05138.1; GSPDB:C  
A:Experimental source: strain ILL403  
C:Genetics:  
A:Gene: p1233

Query Match 19.9%; Score 103; DB 2; Length 397;  
Best Local Similarity 34.1%; Pred. No. 3;  
Matches 31; Conservative 20; Mismatches 32; Indels 8; Gaps 4;

QY 1 LAKQTELEKLDNLDPEGKTQDELKKAELA-BLDKADLPNKVADLEKEISNLE-IL 58  
DB 29 LEKQNDLEERALE-----EAKTDEIEISTVSDADLEKQVLDKELAKQEKODLEDEL 84

QY 59 LGADPEDDTALPNKLTATKAELEKTEL 89  
DB 85 AKAADPTDQKPKDGKRRKKPKV--TEEL 113

RESULT 11  
T18296  
myosin heavy chain - Entamoeba histolytica  
C:Species: Entamoeba histolytica  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
A:Accession: T18296

R:Guillen, N.  
submitted to the EMBL Data Library, February 1997  
A:Reference number: Z18865  
A:Accession: T18296  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-2139 <GUI>  
A:Cross-references: UNIPROT:Q07569; EMBL:L03534; NID:G1850912; PID:G1850913; PIDN:AA84806  
C:Genetics:  
A:Gene: mhca  
C:Superfamily: myosin heavy chain; myosin motor domain homology  
F:91-780/Domain: myosin motor domain homology <MMO>

Query Match 19.5%; Score 101; DB 2; Length 2139;  
Best Local Similarity 30.1%; Pred. No. 24;  
Matches 37; Conservative 23; Mismatches 33; Indels 30; Gaps 6;

QY 2 AKKQTELEKLDNLDPEGKTQDEL-----DKAAAEALDK--KADELPNKV 45  
DB 1485 AKKQSDAD--LEELNKVTEHEDEVAKLNTQITRLTRDQNSAEELNELSKADKDKKI 1542

QY 46 ADLEKEISNLE--ILLGADP-----EDDTALPNKLTATKCA---ELEKTELDAAL 93  
DB 1543 SELEEQVNELEBSRPVGTGNADENEKIKRDAQIADLNPALEWKGVQNNQLQATNKLPAKD 1602

QY 94 NEL 96  
DB 1603 NDL 1605

RESULT 12  
S33068  
myosin heavy chain - fluke (Schistosoma mansoni) (fragment)  
N:Alternate names: surface antigen, 200X  
C:Species: Schistosoma mansoni  
C:Date: 22-Nov-1993 #sequence\_revision 06-Sep-1996 #text\_change 09-Jul-2004  
C:Accession: S33068  
R:Soisson, L.M.A.; Masters, C.P.; Tom, T.D.; McNally, M.T.; Lowell, G.H.; Strand, M.  
J. Immunol. 149, 3612-3620, 1992  
A:Title: Induction of protective immunity in mice using a 62-kDa recombinant fragment of  
A:Reference number: A46514; MUID:93056536; PMID:1431131  
A:Accession: S33068  
A:Molecule type: mRNA  
A:Residues: 1-527 <SOI>  
A:Cross-references: UNIPROT:Q26589; EMBL:X6591  
A:Note: the authors translated the codon CAA for residue 346 as Lys  
C:Superfamily: myosin heavy chain; myosin motor domain homology  
C:Keywords: ATP; surface antigen

Query Match 19.4%; Score 100.5; DB 2; Length 527;  
Best Local Similarity 28.4%; Pred. No. 6.1;  
Matches 31; Conservative 23; Mismatches 40; Indels 15; Gaps 3;

QY 2 AKKQTELEKLDNLDPEGKTQDELKKAELAELDKA-----DELPNKVADLEKEISNLE 56  
DB 308 AKLESTIDEMENLARKQIRGDVEKSRKLEGLKATQETVDLLEVKRDLERQLRKE 367

QY 57 ILLGADP--EDDTALPNKLTATKAELEKTELDAALNGLPGDDEE 103  
DB 368 AEIGSLGKFEDEGLV-----ADLQRIKELQTRIDLEEDLEAE 408

RESULT 13  
A27224  
myosin heavy chain II - Acanthamoeba castellanii  
N:Contains: myosin ATPase (EC 3.6.4.1)  
C:Species: Acanthamoeba castellanii  
C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004  
C:Accession: A27224  
R:Hammer III, J.A.; Bowers, B.; Paterson, B.M.; Korn, E.D.  
J. Cell Biol. 105, 913-925, 1987  
A:Title: Complete nucleotide sequence and deduced polypeptide sequence of a nonmuscle myr  
A:Reference number: A27224; MUID:87308395; PMID:3040773

A:Accession: A27224  
 A:Molecule type: DNA  
 A:Residues: 1-1509 <HAM>  
 A:Cross-references: UNIPROT:P05655; GB:Y00624; GB:M12702; GB:M12703; GB:M19549; NID:9558  
 C:Genetics:  
 A:introns: 69/3; 119/3; 181/2  
 C:Superfamily: myosin heavy chain; myosin motor domain homology  
 C:Keywords: actin binding; ATP; coiled coil; hydrolase; methylated amino acid; nucleotide  
 F:92-775/Domain: myosin motor domain homology <MMOT>  
 F:182-189/Region: nucleotide-binding motif A (P-loop)  
 F:544-576/Region: actin binding #status predicted  
 F:660-682/Region: actin binding #status predicted  
 F:848-1227/Domain: coiled coil #status predicted <COI>  
 F:1228-1247/Domain: hinge <HIN>  
 F:1248-1482/Domain: coiled coil #status predicted <CO2>  
 F:1483-1509/Domain: carboxyl-terminal <CBT>  
 F:133/Modified site: N6,N6,N6-trimethyllysine (Lys) #status predicted  
 F:188/Binding site: ATP (Lys) #status predicted

Query Match 19.4%; Score 100.5; DB 1; Length 1509;  
 Best Local Similarity 31.5%; Pred. No. 18;  
 Matches 39; Conservative 23; Mismatches 31; Indels 31; Gaps 6;

QY 5 QTELEKLDNDPEGKTODELDKKA-----AAELDKK-----ADELPNKVADLEKEI 52  
 DB 851 QNRFOKEIDDLKKQVK---DLEKELAAKQANAKLDKEKQAEADADKLEKDLAAKTKI 907

QY 53 SNIEILGG--ADPEDDTAALPNKLTATKKAEL-----KTQKELDALNELGPDG 100  
 DB 908 LDLE-----GEKADLEEDNALQKKVAGLEBELQETSASNDILEQRKLEAKEGELKASL 963

QY 101 DEEE 104  
 DB 964 EEE 967

RESULT 14  
 A59287  
 myosin heavy chain - fluke (Schistosoma mansoni) (strain Brazilian LE)  
 C:Species: Schistosoma mansoni  
 C:Date: 09-Jun-2000 #sequence\_revision 09-Jun-2000 #text\_change 09-Jul-2004  
 C:Accession: A59287  
 R:Weston, D.S.; Schmitz, J.; Kemp, M.; Kunz, W.  
 M:J. Biochem. Parasitol. 58, 161-164, 1993  
 A:Title: Cloning and sequence characterization of a complete myosin heavy chain cDNA from  
 A:Reference number: A59287; MUID:93211444; PMID:8459827  
 A:Accession: A59287  
 A:Status: preliminary; not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 1-1940 <MES>  
 A:Cross-references: UNIPROT:Q02456; GB:L01634; PIDN:AAA29905.1  
 A:Experimental source: strain Brazilian LE  
 C:Genetics:  
 A:Gene: MYH  
 C:Superfamily: myosin heavy chain; myosin motor domain homology  
 F:82-752/Domain: myosin motor domain homology <MMO>

Query Match 19.4%; Score 100.5; DB 2; Length 1940;  
 Best Local Similarity 28.4%; Pred. No. 23;  
 Matches 31; Conservative 23; Mismatches 40; Indels 15; Gaps 3;

QY 2 AKQTELEKLDNDPEGKTODELDKKAELADKKA-----DELPNKVADLEKEISNLE 56  
 DB 1011 AKLESTLDEMEENLAEQKTRGVESKRLTEGLDKATQETVDDLERYKRDLEELRKE 1070

QY 57 ILLGGADP--EDDTALPNKLTATKKAELKTOKELDALNELGPDGDE 103  
 DB 1071 AELGSLGKPEDEGLV-----AQLQKIKELQTRIOLEEDLEAE 1111

RESULT 15  
 D60110  
 repetitive protein antigen 3 - Trypanosoma cruzi (fragment)

C:Species: Trypanosoma cruzi  
 C:Date: 10-Nov-1992 #sequence\_revision 10-Nov-1992 #text\_change 09-Jul-2004  
 C:Accession: D60110  
 R:Hofc, D.F.; Kim, K.S.; Otsu, K.; Moser, D.R.; Yost, W.J.; Blumin, J.H.; Donelson, J.E.  
 Infect. Immun. 57, 1959-1967, 1989  
 A:Title: Trypanosoma cruzi expresses diverse repetitive protein antigens.  
 A:Reference number: A60110; MUID:89277508; PMID:2659529  
 A:Accession: D60110  
 A:Status: not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 1-259 <HOF>  
 A:Cross-references: UNIPROT:Q7M3R6  
 C:Keywords: tandem repeat  
 F:2-99/Region: 14-residue repeats

Query Match 19.3%; Score 100; DB 2; Length 259;  
 Best Local Similarity 34.3%; Pred. No. 3.1;  
 Matches 34; Conservative 16; Mismatches 35; Indels 14; Gaps 4;

QY 3 KKQTELEKLDNDPEG-----KTQELDKKAELADKKADELPMNKVADLEKEISNLE 58  
 DB 2 QKAENERLADLEEQKAAENERLADLEEQTAENE--RLADLEQKAAENERLADLE 57

QY 59 LGGADPEDDTAALPNKLTATKKAELKTOKELD--AALNE 95  
 DB 58 ----QKAENERLADLEEQKAAENERLADLEEQKAAENE 92

Search completed: November 19, 2004, 22:36:10  
 Job time : 14.9512 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 19, 2004, 21:57:48 ; Search time 72.8211 Seconds  
(without alignments)  
821.725 Million cell updates/sec

Title: US-10-674-755-21

Perfect score: 518  
Sequence: 1 LAKKQTELEKLDNDPEBK.....TQKELDALNELGPDGDEE 104

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt 02:.\*  
1: uniprot\_sprot:.\*  
2: uniprot\_trembl:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	502	96.9	231	2	Q9L579 streptococc
2	502	96.9	241	2	Q9L580 streptococc
3	498	96.1	502	2	Q9LAX8 streptococc
4	492	95.0	249	2	Q9L5B7 streptococc
5	491	94.8	249	2	Q9L585 streptococc
6	491	94.8	256	2	Q9L590 streptococc
7	484	93.4	209	2	Q9L593 streptococc
8	484	93.4	228	2	Q9L5B8 streptococc
9	484	93.4	235	2	Q9L582 streptococc
10	484	93.4	249	2	Q9L5D4 streptococc
11	484	93.4	252	2	Q9L583 streptococc
12	484	93.4	360	2	Q8KOK3 streptococc
13	484	93.4	429	2	Q9LAX7 streptococc
14	484	93.4	526	2	Q9LAX9 streptococc
15	484	93.4	608	2	Q8V055 streptococc
16	484	93.4	744	2	Q9L562 streptococc
17	475	91.7	242	2	Q9L584 streptococc
18	466	90.0	222	2	Q9L5B4 streptococc
19	326	62.9	246	2	Q9L584 streptococc
20	322	62.2	479	2	Q9LAX2 streptococc
21	322	62.2	481	2	Q9LAX5 streptococc
22	321	62.0	107	2	Q8KOK2 streptococc
23	315	60.8	653	2	Q34097 streptococc
24	310	59.8	213	2	Q8GNS7 streptococc
25	297	57.3	480	2	Q9LAX3 streptococc
26	252.5	48.7	211	2	Q8GNT0 streptococc
27	252.5	48.7	257	2	Q9L594 streptococc
28	245.5	47.4	227	2	Q9KGS0 streptococc
29	245.5	47.4	256	2	Q9L595 streptococc
30	245.5	47.4	461	2	Q9LAX6 streptococc
31	139	26.8	417	2	Q9LAX3 streptococc

32	130	25.1	415	2	Q9LAV1 streptococc
33	129.5	25.0	222	2	Q9L577 streptococc
34	129.5	25.0	262	2	Q9L576 streptococc
35	129.5	25.0	415	2	Q9LAV7 streptococc
36	128.5	24.8	237	2	Q9L592 streptococc
37	128.5	24.8	255	2	Q9L581 streptococc
38	128.5	24.8	255	2	Q9L5B6 streptococc
39	128.5	24.8	395	2	Q9LAV9 streptococc
40	128.5	24.8	416	2	Q9LAV8 streptococc
41	128	24.7	249	2	Q9L575 streptococc
42	128	24.7	619	2	Q54972 streptococc
43	128	24.7	739	2	Q8DR10 streptococc
44	127	24.5	739	2	Q9RQT4 streptococc
45	127	24.5	820	2	Q9RQT1 streptococc

## ALIGNMENTS

RESULT 1					
ID	Q9L579	PRELIMINARY;	PRT;	231 AA.	
AC	Q9L579;				
DT	01-OCT-2000 (Tremblrel. 15, Created)				
DT	01-OCT-2000 (Tremblrel. 15, Last sequence update)				
DE	01-MAR-2004 (Tremblrel. 26, Last annotation update)				
DE	Pspa (Fragment).				
GN	Name=pspa;				
OS	Streptococcus pneumoniae.				
OC	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;				
OC	Streptococcus.				
OX	NCBI_Taxid=1313;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=20;				
RX	MEDLINE=20472698; PubMed=11015380;				
RA	Beall B., Gherardi G., Facklam R.R., Hollingshead S.K.;				
RT	"Pneumococcal pspsa sequence types of prevalent multiresistant				
RT	pneumococcal strains in the United States and of internationally				
RT	disseminated clones.";				
RL	J. Clin. Microbiol. 38:3663-3669(2000).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=20;				
RA	Beall B.W.;				
RL	Submitted (Apr-2000) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AF255548; AAF68101.1; --				
FT	NON TER				
FT	1				
FT	231				
SO	SEQUENCE 231 AA; 24990 MW; A7731F3A46460186 CRC64;				
Query Match					
Best Local Similarity 96.9%; Score 502; DB 2; Length 231;					
Matches 102; Conservative 0; Mismatches 2; Indels 0; Gaps 0;					
QY	1 LAKKQTELEKLDNDPEBKTDDELDEKAAEELDKKADLEPNKYADLEKESINLEITLG 60				
DB	76 LAKKQTELEKLDNDPEBKTDDELDEKAAEELDKKADLEPNKYADLEKESINLEITLG 135				
QY	61 GADPEDDTAALPNKATKAELEKTKQKELDALNELGPDGDEE 104				
DB	136 GADPEDDTAALPNKATKAELEKTKQKELDALNELGPDGDEE 179				
RESULT 2					
ID	Q9L580	PRELIMINARY;	PRT;	241 AA.	
AC	Q9L580;				
DT	01-OCT-2000 (Tremblrel. 15, Created)				
DT	01-OCT-2000 (Tremblrel. 15, Last sequence update)				
DT	01-MAR-2004 (Tremblrel. 26, Last annotation update)				
DE	Pspa (Fragment).				
GN	Name=pspa;				

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OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCB1_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=121;
RX MEDLINE=20472698; PubMed=11015380;
RA Beall B., Gherardi G., Facklam R.R., Hollingshead S.K.;
RT "Pneumococcal pspa sequence types of prevalent multiresistant
RT pneumococcal strains in the United States and of internationally
RT disseminated clones.";
RL J. Clin. Microbiol. 38:3663-3669(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=121;
RX Beall B.W.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF255547; AAF68100.1; -.
FT NON TER 1 1
SQ SEQUENCE 241 AA; 26038 MW; BB87E1A4C5F5A669 CRC64;

Query Match 96.9%; Score 502; DB 2; Length 241;
Best Local Similarity 98.1%; Pred. No. 3.5e-26;
Matches 102; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Cy 1 LAKKQTELEKLDNDPEGKTQDELDKAABAEIDKKADELPNKVADLEKEISNLEITLG 60
Db 77 LAKKQTELEKLDNDPEGKTQDELDKAABAEIDKKADELPNKVADLEKEISNLEITLG 136
61 GADPEDDTAALPNKLTATKKALEKTKQKELDPAALNELGPDGDEE 104
137 GADPEDDTAALQNKLTATKKALEKTKQKELDPAALNELGPDGDEE 180

RESULT 3
ID Q9LAX8 PRELIMINARY; PRT; 502 AA.
AC Q9LAX8;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Pspa (Fragment).
GN Name=pspa;
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCB1_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BG8090;
RX MEDLINE=20448953; PubMed=10992499;
RA Hollingshead S.K., Becker R., Briles D.E.;
RT "Diversity of Pspa: mosaic genes and evidence for past recombination
RT in Streptococcus pneumoniae.";
RL Infect. Immun. 68:5889-5900(2000).
DR EMBL; AF071817; AAF27713.1; -.
DR InterPro; IPR000533; Tropomyosin.
DR PRINTS; PRO0194; TROPOMIOSIN.
FT NON TER 502 502
SQ SEQUENCE 502 AA; 55018 MW; 4E73D477CAE79B40 CRC64;

Query Match 96.1%; Score 498; DB 2; Length 502;
Best Local Similarity 97.1%; Pred. No. 1.3e-25;
Matches 101; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Cy 1 LAKKQTELEKLDNDPEGKTQDELDKAABAEIDKKADELPNKVADLEKEISNLEITLG 50
Db 347 LAKKQTELEKLDNDPEGKTQDELDKAABAEIDKKADELPNKVADLEKEISNLEITLG 406
61 GADPEDDTAALPNKLTATKKALEKTKQKELDPAALNELGPDGDEE 104
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Db 407 GADPEDDTAALQNKLTATKKALEKTKQKELDPAALNELGPDGDEE 450

RESULT 4
ID Q9LSB7 PRELIMINARY; PRT; 249 AA.
AC Q9LSB7;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Pspa (Fragment).
GN Name=pspa;
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCB1_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=50;
RX MEDLINE=20472698; PubMed=11015380;
RA Beall B., Gherardi G., Facklam R.R., Hollingshead S.K.;
RT "Pneumococcal pspa sequence types of prevalent multiresistant
RT pneumococcal strains in the United States and of internationally
RT disseminated clones.";
RL J. Clin. Microbiol. 38:3663-3669(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=50;
RX Beall B.W.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF253405; AAF67353.1; -.
FT NON TER 1 1
SQ SEQUENCE 249 AA; 27271 MW; B4106707EF108A0B CRC64;

Query Match 95.0%; Score 492; DB 2; Length 249;
Best Local Similarity 96.2%; Pred. No. 1.7e-25;
Matches 100; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Cy 1 LAKKQTELEKLDNDPEGKTQDELDKAABAEIDKKADELPNKVADLEKEISNLEITLG 60
Db 103 LAKKQTELEKLDNDPEGKTQDELDKAABAEIDKKADELPNKVADLEKEISNLEITLG 162
61 GADPEDDTAALPNKLTATKKALEKTKQKELDPAALNELGPDGDEE 104
163 GADPEDDTAALQNKLTATKKALEKTKQKELDPAALNELGPDGDEE 206

RESULT 5
ID Q9LS85 PRELIMINARY; PRT; 249 AA.
AC Q9LS85;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Pspa (Fragment).
GN Name=pspa;
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCB1_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=18;
RX MEDLINE=20472698; PubMed=11015380;
RA Beall B., Gherardi G., Facklam R.R., Hollingshead S.K.;
RT "Pneumococcal pspa sequence types of prevalent multiresistant
RT pneumococcal strains in the United States and of internationally
RT disseminated clones.";
RL J. Clin. Microbiol. 38:3663-3669(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=18;
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RA Beall B.W.;  
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF255542; AAF68095.1; -  
 FT NON\_TER 1  
 FT NON\_TER 249  
 SQ SEQUENCE 249 AA; 27050 MW; DFAD2BD9265986FA CRC64;

Query Match 94.8%; Score 491; DB 2; Length 249;  
 Best Local Similarity 96.2%; Pred. No. 2e-25;  
 Matches 100; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 LAKKOTELKLDNLDPEKGTODELDKKAABAEALDKKADLPNKVADLEKEISNLEILLG 60  
 DB 68 LAKKOTELKLDNLDPEKGTODELDKKAABAEALDKKADLPNKVADLEKEISNLEILLG 127

QY 61 GADPEDDTAALPNKLTATKKALEKTOKELDALALNELGPDGDEE 104  
 DB 128 GADPEDDTAALPNKLTATKKALEKTOKELDALALNELGPDGDEE 171

## RESULT 6

ID Q9L590 PRELIMINARY; PRT; 256 AA.

AC Q9L590;  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
 DE Psppa (Fragment).  
 GN Name=psppa;  
 OS Streptococcus pneumoniae.  
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
 OC Streptococcus.  
 OX NCBI\_TaxID=1313;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SP193;  
 RX MEDLINE=20472698; PubMed=11015380;

RA Beall B., Cherard G., Packiam R.R., Hollingshead S.K.;  
 "Pneumococcal psppa sequence types of prevalent multiresistant  
 RT pneumococcal strains in the United States and of internationally  
 RT disseminated clones."  
 RL J. Clin. Microbiol. 38:3663-3669(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SP193;  
 RA Beall B.W.;  
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF254259; AAF68094.1; -  
 FT NON\_TER 1  
 FT NON\_TER 256  
 SQ SEQUENCE 256 AA; 27738 MW; 7F05351559AD9238 CRC64;

Query Match 94.8%; Score 491; DB 2; Length 256;  
 Best Local Similarity 96.2%; Pred. No. 2e-25;  
 Matches 100; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 LAKKOTELKLDNLDPEKGTODELDKKAABAEALDKKADLPNKVADLEKEISNLEILLG 60  
 DB 66 LAKKOTELKLDNLDPEKGTODELDKKAABAEALDKKADLPNKVADLEKEISNLEILLG 125

QY 61 GADPEDDTAALPNKLTATKKALEKTOKELDALALNELGPDGDEE 104  
 DB 126 GADPEDDTAALPNKLTATKKALEKTOKELDALALNELGPDGDEE 169

## RESULT 7

ID Q9L593 PRELIMINARY; PRT; 209 AA.

AC Q9L593;  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
 DE Psppa (Fragment).

GN Name=psppa;  
 OS Streptococcus pneumoniae.  
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
 OC Streptococcus.  
 OX NCBI\_TaxID=1313;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=115;  
 RX MEDLINE=20472698; PubMed=11015380;

RA Beall B., Cherard G., Packiam R.R., Hollingshead S.K.;  
 "Pneumococcal psppa sequence types of prevalent multiresistant  
 RT pneumococcal strains in the United States and of internationally  
 RT disseminated clones."  
 RL J. Clin. Microbiol. 38:3663-3669(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=115;  
 RA Beall B.W.;  
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF254256; AAF68091.1; -  
 FT NON\_TER 1  
 FT NON\_TER 209  
 SQ SEQUENCE 209 AA; 22628 MW; 06FF588F7C3BD5B7 CRC64;

Query Match 93.4%; Score 484; DB 2; Length 209;  
 Best Local Similarity 95.2%; Pred. No. 4.9e-25;  
 Matches 99; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 LAKKOTELKLDNLDPEKGTODELDKKAABAEALDKKADLPNKVADLEKEISNLEILLG 60  
 DB 19 LAKKOTELKLDNLDPEKGTODELDKKAABAEALDKKADLPNKVADLEKEISNLEILLG 78

QY 61 GADPEDDTAALPNKLTATKKALEKTOKELDALALNELGPDGDEE 104  
 DB 79 GADPEDDTAALPNKLTATKKALEKTOKELDALALNELGPDGDEE 122

## RESULT 8

ID Q9L5B8 PRELIMINARY; PRT; 228 AA.

AC Q9L5B8;  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
 DE Psppa (Fragment).  
 GN Name=psppa;  
 OS Streptococcus pneumoniae.  
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
 OC Streptococcus.  
 OX NCBI\_TaxID=1313;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=60;  
 RX MEDLINE=20472698; PubMed=11015380;

RA Beall B., Cherard G., Packiam R.R., Hollingshead S.K.;  
 "Pneumococcal psppa sequence types of prevalent multiresistant  
 RT pneumococcal strains in the United States and of internationally  
 RT disseminated clones."  
 RL J. Clin. Microbiol. 38:3663-3669(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=60;  
 RA Beall B.W.;  
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF253404; AAF67352.1; -  
 FT NON\_TER 1  
 FT NON\_TER 228  
 SQ SEQUENCE 228 AA; 24430 MW; E6EA953BC54EA0F CRC64;

Query Match 93.4%; Score 484; DB 2; Length 228;  
 Best Local Similarity 95.2%; Pred. No. 5.3e-25;  
 Matches 99; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

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QY 1 LAKKQTELEKLDNLDPEGKTQDELDKAAEAELDKKADBLPNKVADLEKEISNLEITLG 60
   |||||
DB 46 LAKKQTELEKLDNLDPEGKTQDELDKAAEAELDKKADBLQNKVADLEKEISNLEITLG 105
   |||||
QY 61 GADPEDDTAALPNKLTATKKALEKTKQKELDAALNELGPDGDEE 104
   |||||
DB 106 GADSEDDTAALQNKLTATKKALEKTKQKELDAALNELGPDGDEE 149
   |||||

RESULT 9
Q9L582 PRELIMINARY; PRT; 235 AA.
ID Q9L582;
AC Q9L582;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Psppa (Fragment).
GN Name=psppa;
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3;
RX MEDLINE=20472698; PubMed=11015380;
RA Beall B., Gherardi G., Packlam R.R., Hollingshead S.K.;
RT "Pneumococcal psppa sequence types of prevalent multiresistant
RT pneumococcal strains in the United States and of internationally
RT disseminated clones.";
RL J. Clin. Microbiol. 38:3663-3669(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=3;
RA Beall B.W.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF255545; AAF68098.1; -.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 235 AA; 25424 MW; BFFBBA8C52CA8380 CRC64;

Query Match 93.4%; Score 484; DB 2; Length 235;
Best Local Similarity 95.2%; Pred. No. 5.5e-25;
Matches 99; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 LAKKQTELEKLDNLDPEGKTQDELDKAAEAELDKKADBLPNKVADLEKEISNLEITLG 60
   |||||
DB 56 LAKKQTELEKLDNLDPEGKTQDELDKAAEAELDKKADBLQNKVADLEKEISNLEITLG 115
   |||||
QY 61 GADPEDDTAALPNKLTATKKALEKTKQKELDAALNELGPDGDEE 104
   |||||
DB 116 GADSEDDTAALQNKLTATKKALEKTKQKELDAALNELGPDGDEE 159
   |||||

RESULT 10
Q9L5D4 PRELIMINARY; PRT; 249 AA.
ID Q9L5D4;
AC Q9L5D4;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Psppa (Fragment).
GN Name=psppa;
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SP195;
RX MEDLINE=20472698; PubMed=11015380;
RA Beall B., Gherardi G., Packlam R.R., Hollingshead S.K.;
RT "Pneumococcal psppa sequence types of prevalent multiresistant

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RT pneumococcal strains in the United States and of internationally
RT disseminated clones.";
RL J. Clin. Microbiol. 38:3663-3669(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SP195;
RA Beall B.W.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF252286; AAF69499.1; -.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 249 AA; 26821 MW; F8EA39225CF8D43F CRC64;

Query Match 93.4%; Score 484; DB 2; Length 249;
Best Local Similarity 95.2%; Pred. No. 5.8e-25;
Matches 99; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 LAKKQTELEKLDNLDPEGKTQDELDKAAEAELDKKADBLPNKVADLEKEISNLEITLG 60
   |||||
DB 67 LAKKQTELEKLDNLDPEGKTQDELDKAAEAELDKKADBLQNKVADLEKEISNLEITLG 126
   |||||
QY 61 GADPEDDTAALPNKLTATKKALEKTKQKELDAALNELGPDGDEE 104
   |||||
DB 127 GADSEDDTAALQNKLTATKKALEKTKQKELDAALNELGPDGDEE 170
   |||||

RESULT 11
Q9L583 PRELIMINARY; PRT; 252 AA.
ID Q9L583;
AC Q9L583;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Psppa (Fragment).
GN Name=psppa;
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=127;
RX MEDLINE=20472698; PubMed=11015380;
RA Beall B., Gherardi G., Packlam R.R., Hollingshead S.K.;
RT "Pneumococcal psppa sequence types of prevalent multiresistant
RT pneumococcal strains in the United States and of internationally
RT disseminated clones.";
RL J. Clin. Microbiol. 38:3663-3669(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=127;
RA Beall B.W.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF255544; AAF68097.1; -.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 252 AA; 27260 MW; 82DE13741F369CA2 CRC64;

Query Match 93.4%; Score 484; DB 2; Length 252;
Best Local Similarity 95.2%; Pred. No. 5.9e-25;
Matches 99; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 LAKKQTELEKLDNLDPEGKTQDELDKAAEAELDKKADBLPNKVADLEKEISNLEITLG 60
   |||||
DB 73 LAKKQTELEKLDNLDPEGKTQDELDKAAEAELDKKADBLQNKVADLEKEISNLEITLG 132
   |||||
QY 61 GADPEDDTAALPNKLTATKKALEKTKQKELDAALNELGPDGDEE 104
   |||||
DB 133 GADSEDDTAALQNKLTATKKALEKTKQKELDAALNELGPDGDEE 176
   |||||

RESULT 12
Q8XOK3

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ID Q8OK3 PRELIMINARY; PRT; 360 AA.  
 AC Q8OK3;  
 DT 01-OCT-2002 (TREMBlrel. 22, Created)  
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)  
 DE 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DB Pneumococcal surface protein A (Fragment).  
 GN Name=papA;  
 OS Streptococcus pneumoniae.  
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
 OC Streptococcus.  
 NCBI\_TaxID=1313;  
 OX NCBI\_TaxID=1313;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=259/98;  
 RX MEDLINE=22170754; PubMed=12183557;  
 RA Miyaji E.N., Ferreira D.M., Lopes A.P.Y., Brandilione M.C.C.,  
 Dias W.O., Leite L.C.C.;  
 RT "Analysis of serum cross-reactivity and cross-protection elicited by  
 immunization with DNA vaccines against Streptococcus pneumoniae  
 expressing PapA fragments from different clades.";  
 RT Infect. Immun. 70:5086-5090(2002).  
 RL Infect. Immun. 70:5086-5090(2002).  
 DR EMBL; AF082389; AAL92494.1;  
 DR InterPro; IPR000533; Tropomyosin.  
 DR PRINTS; PR00194; TROPOMYOSIN.  
 FT NON\_TER 1 1  
 FT NON\_TER 360 360  
 SQ SEQUENCE 360 AA; 39575 MW; 0C09A791547A7EC CRC64;

Query Match 93.4%; Score 484; DB 2; Length 360;  
 Best Local Similarity 95.2%; Pred. No. 8.4e-25;  
 Matches 99; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 LAKKQTELEKLDNDLDPGKTDDELDEKAEAEALDKKADLPNKVADLEKEISNLEILLG 60  
 DB 232 LAKKQTELEKLDNDLDPGKTDDELDEKAEAEALDKKADLPNKVADLEKEISNLEILLG 291  
 QY 61 GADPEDDTAALPNKATKKALEKTKQKELDAALNLELGPDDDEE 104  
 DB 292 GADSEDDTAALQNKLATKKALEKTKQKELDAALNLELGPDDDEE 335

RESULT 13  
 Q9LAX7 PRELIMINARY; PRT; 429 AA.

AC Q9LAX7;  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
 DE PapA (Fragment).  
 GN Name=papA;  
 OS Streptococcus pneumoniae.  
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
 OC Streptococcus.  
 NCBI\_TaxID=1313;  
 OX NCBI\_TaxID=1313;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=AC122;  
 RX MEDLINE=20448953; PubMed=10992499;  
 RA Hollingshead S.K., Becker R., Biles D.E.;  
 RT "Diversity of PapA: mosaic genes and evidence for past recombination  
 in Streptococcus pneumoniae.";  
 RT Infect. Immun. 68:5889-5900(2000).  
 RL Infect. Immun. 68:5889-5900(2000).  
 DR EMBL; AF071818; AAF27714.1;  
 DR InterPro; IPR011009; Kinase\_like.  
 DR InterPro; IPR000533; Tropomyosin.  
 DR PRINTS; PR00194; TROPOMYOSIN.  
 FT NON\_TER 429 429  
 SQ SEQUENCE 429 AA; 47048 MW; BCID74BBA54DA9D6 CRC64;

Query Match 93.4%; Score 484; DB 2; Length 429;  
 Best Local Similarity 95.2%; Pred. No. 1e-24;  
 Matches 99; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 LAKKQTELEKLDNDLDPGKTDDELDEKAEAEALDKKADLPNKVADLEKEISNLEILLG 60  
 DB 254 LAKKQTELEKLDNDLDPGKTDDELDEKAEAEALDKKADLPNKVADLEKEISNLEILLG 313  
 QY 61 GADPEDDTAALPNKATKKALEKTKQKELDAALNLELGPDDDEE 104  
 DB 314 GADSEDDTAALQNKLATKKALEKTKQKELDAALNLELGPDDDEE 357

RESULT 14

Q9LAX9 PRELIMINARY; PRT; 526 AA.

AC Q9LAX9;  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
 DE PapA (Fragment).  
 GN Name=papA;  
 OS Streptococcus pneumoniae.  
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
 OC Streptococcus.  
 NCBI\_TaxID=1313;  
 OX NCBI\_TaxID=1313;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=EF3296;  
 RX MEDLINE=20448953; PubMed=10992499;  
 RA Hollingshead S.K., Becker R., Biles D.E.;  
 RT "Diversity of PapA: mosaic genes and evidence for past recombination  
 in Streptococcus pneumoniae.";  
 RT Infect. Immun. 68:5889-5900(2000).  
 DR EMBL; AF071816; AAF27712.1;  
 DR InterPro; IPR011009; Kinase\_like.  
 FT NON\_TER 526 526  
 FT NON\_TER 526 526  
 SQ SEQUENCE 526 AA; 58106 MW; 5F1F564A2CB678AE CRC64;

Query Match 93.4%; Score 484; DB 2; Length 526;  
 Best Local Similarity 95.2%; Pred. No. 1.2e-24;  
 Matches 99; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 LAKKQTELEKLDNDLDPGKTDDELDEKAEAEALDKKADLPNKVADLEKEISNLEILLG 60  
 DB 346 LAKKQTELEKLDNDLDPGKTDDELDEKAEAEALDKKADLPNKVADLEKEISNLEILLG 405  
 QY 61 GADPEDDTAALPNKATKKALEKTKQKELDAALNLELGPDDDEE 104  
 DB 406 GADSEDDTAALQNKLATKKALEKTKQKELDAALNLELGPDDDEE 449

RESULT 15

Q8VO55 PRELIMINARY; PRT; 608 AA.

AC Q8VO55;  
 DT 01-MAR-2002 (TREMBlrel. 20, Created)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)  
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
 DE Pneumococcal surface protein A (Fragment).  
 GN Name=papA;  
 OS Streptococcus pneumoniae.  
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
 OC Streptococcus.  
 NCBI\_TaxID=1313;  
 OX NCBI\_TaxID=1313;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=KNH1156;  
 RX Lee K.J., Bae S.M., Chung K.S.;  
 RT Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
 RL EMBL; AF460993; AAL67804.1;  
 DR InterPro; IPR002479; CW\_binding.  
 DR InterPro; IPR002479; CW\_binding.  
 DR Pfam; PF01473; CW\_binding\_1; 10.  
 DR PROSITE; PS00213; LIPOCALIN; UNKNOWN\_2.  
 FT NON\_TER 608 608

SQ SEQUENCE 608 AA; 67918 MW; 15F71BD62E297526 CRC64;

Query Match	93.4%;	Score 484;	DB 2;	Length 608;
Best Local Similarity	95.3%;	Prod No 1	46-24.	

Matches 99; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

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001 LAKKOTELKULDNIDPEKKODELDEAFAEELDKADELNNKVALEKEISNLEITLG 60
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022 LAKKOTELKULDSLPDEKKODELDEKAEEAEFLDKADELQNKVALEKEISNLEITLG 281
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Search completed: November 19, 2004, 22:31:53  
Job time : 72.8211 secs